

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 18:53:48 ; Search time 4.24897 Seconds
(without alignments)
1034.083 Million cell updates/sec

Title: US-10-525-567-1
Perfect score: 49
Sequence: 1 AAVNHQKSA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Match	Length	DB ID	Description
1	49	100.0	10	8	ADL27604 Honey bee
2	49	100.0	524	8	ADL27606 Honey bee
3	49	100.0	544	8	ADL27618 Honey bee
4	49	100.0	544	8	ADL27616 Honey bee
5	36	73.5	347	4	ABb64181 Drosophil
6	36	73.5	503	4	ABb63773 Drosophil
7	36	73.5	599	4	ABg14172 Novel hum
8	36	73.5	599	4	AAU32811 Novel hum
9	35	71.4	535	6	AAU40932 Propionib
10	35	71.4	535	6	ABm37451 Propionib
11	35	71.4	664	7	ADD31051 Plant yie
12	35	71.4	664	8	ADL44067 Plant tra
13	35	71.4	5509	8	ADN96832 Bugula br
14	35	71.4	6940	8	ADN96829 Bugula br
15	34	69.4	284	8	ADS30840 Bacterial
16	34	69.4	291	4	ABg07730 Novel hum
17	34	69.4	300	4	ABg14415 Novel hum
18	34	69.4	307	6	ABm67540 Photorhab
19	34	69.4	387	5	ABp69562 Human pol
20	34	69.4	445	4	ABg05552 Novel hum
21	34	69.4	453	4	ABg14171 Novel hum
22	34	69.4	454	4	ABg06133 Novel hum
23	34	69.4	479	2	AAR99230 Barley xy
24	34	69.4	562	8	ADQ67724 Novel hum

25	34	69.4	604	9	AEA20216	Aea20216 Novel hum
26	33	67.3	71	4	AAU64987	Aau64987 Propionib
27	33	67.3	71	6	ABM61506	Abm61506 Propionib
28	33	67.3	250	6	ABU20971	Abu20971 Protein e
29	33	67.3	291	4	ABG08383	Abg08383 Novel hum
30	33	67.3	375	4	ABB68042	Abb68042 Drosophil
31	33	67.3	380	4	AAU32883	Aau32883 Novel hum
32	33	67.3	809	6	ABP77288	Abp77288 N. gonorr
33	33	67.3	810	9	AEb91535	Aeb91535 Microbial
34	33	67.3	1103	8	ADq67756	Adq67756 Novel hum
35	33	67.3	3572	5	ABg95659	Abg95659 Human nuc
36	32	65.3	53	4	AAU09275	Aau09275 Human pol
37	32	65.3	66	4	AAU66448	Aau66448 Propionib
38	32	65.3	66	6	ABM62967	Abm62967 Propionib
39	32	65.3	71	4	ABG03124	Abg03124 Novel hum
40	32	65.3	77	8	ADK48037	Adk48037 Streptoco
41	32	65.3	79	4	AAU54537	Aau54537 Propionib
42	32	65.3	79	6	ABM51056	Abm51056 Propionib
43	32	65.3	83	4	ABG26402	Abg26402 Novel hum
44	32	65.3	242	9	ABM94288	Abm94288 M. xanthu
45	32	65.3	249	7	ADC97121	Adc97121 E. faeciu

ALIGNMENTS

RESULT 1
ADL27604
ID ADL27604 standard; peptide; 10 AA.
XX AC ADL27604;
XX DT 03-JUN-2004 (first entry)
XX DE Honey bee RJP70 N-terminal peptide, SEQ ID 1.
XX KW Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
XX KW royal jelly protein; allergy; pollinosis; atopic dermatitis;
XX KW contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP70.
XX OS Apis mellifera.
XX PN WO2004019971-A1.
XX PD 11-MAR-2004.
XX PF 26-AUG-2003; 2003WO-JP010795.
XX PR 29-AUG-2002; 2002JP-00252087.
XX PR 30-JAN-2003; 2003JP-00022776.
XX PR (HAYA/) HAYASHIBARA K.
XX PI Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;
XX WPI; 2004-248191/23.

Antiallergic agents for relieving symptoms accompanying e.g. pollinosis, atopic dermatitis, contact hypersensitivity, bronchial asthma and allergic rhinitis, comprise protein originated from royal jelly.
Claim 1; SEQ ID NO 1; 78pp; Japanese.
The present invention relates to novel antiallergic agents, which comprise as an active ingredient, peptides ADL27604 and ADL27605, which are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606 and ADL27607). The agents can be used to relieve symptoms accompanying an allergic disease e.g. pollinosis, atopic dermatitis, contact hypersensitivity, bronchial asthma and allergic rhinitis, which are applicable in foods, cosmetics and drugs.
Sequence 10 AA;

```

Query Match      100.0%; Score 49; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVNHQRKSA 10
Db 1 AAVNHQRKSA 10
|||||

RESULT 2
ADL27606
ID ADL27606 standard; protein; 524 AA.
XX AC ADL27606;
XX XX
XX 03-JUN-2004 (first entry)
XX DE Honey bee RJP70 mature protein, SEQ ID 3.
XX KW Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
XX KW royal jelly protein; allergy; pollinosis; atopic dermatitis;
XX KW contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP70.
XX OS Apis mellifera.
XX PN WO2004019971-A1.
XX PD 11-MAR-2004.
XX PF 26-AUG-2003; 2003WO-JP010795.
XX PR 29-AUG-2002; 2002JP-00252087.
XX PR 30-JAN-2003; 2003JP-00022776.
XX PA (HAYA/) HAYASHIBARA K.
XX PI Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;
XX DR WPI; 2004-248191/23.
XX DR N-PSDB; ADL27608.
XX PT Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,
XX PT atopic dermatitis, contact hypersensitivity, bronchial asthma and
XX PT allergic rhinitis, comprise protein originated from royal jelly.
XX PS Claim 1; SEQ ID NO 3; 78pp; Japanese.
XX CC The present invention relates to novel antiallergic agents, which
XX CC comprise as an active ingredient, peptides ADL27604 and ADL27605, which
XX CC are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606
XX CC and ADL27607). The agents can be used to relieve symptoms accompanying an
XX CC allergic disease e.g. pollinosis, atopic dermatitis, contact
XX CC hypersensitivity, bronchial asthma and allergic rhinitis, which are
XX CC applicable in foods, cosmetics and drugs.
XX SQ Sequence 524 AA;

Query Match      100.0%; Score 49; DB 8; Length 524;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVNHQRKSA 10
Db 1 AAVNHQRKSA 10
|||||

RESULT 3
ADL27618
ID ADL27618 standard; protein; 544 AA.
XX AC ADL27618;
XX XX
XX 03-JUN-2004 (first entry)
XX DT

Query Match      100.0%; Score 49; DB 8; Length 544;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVNHQRKSA 10
Db 21 AAVNHQRKSA 30
|||||

RESULT 4
ADL27616
ID ADL27616 standard; protein; 544 AA.
XX AC ADL27616;
XX XX
XX 03-JUN-2004 (first entry)
XX DE Honey bee RJP70.
XX KW Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
XX KW royal jelly protein; allergy; pollinosis; atopic dermatitis;
XX KW contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP70.
XX OS Apis mellifera.

```

PH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Signal_peptide
FT Protein 21..544
FT /label= Mature_protein
XX WO2004019971-A1.
XX 11-MAR-2004.
XX 26-AUG-2003; 2003WO-JP010795.
XX 29-AUG-2002; 2002JP-00252087.
PR 30-JAN-2003; 2003JP-00022776.
XX (HAYA/) HAYASHIBARA K.
XX Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;
XX WPI; 2004-248191/23.
DR N-PSDB; ADL27608.
XX Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,
PT atopic dermatitis, contact hypersensitivity, bronchial asthma and
PT allergic rhinitis, comprise protein originated from royal jelly.
XX Disclosure; Page 59-62; 78pp; Japanese.
PS The present invention relates to novel antiallergic agents, which
CC comprise as an active ingredient, peptides ADL27604 and ADL27605, which
CC are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606
CC and ADL27607). The agents can be used to relieve symptoms accompanying an
CC allergic disease e.g. pollinosis, atopic dermatitis, contact
CC hypersensitivity, bronchial asthma and allergic rhinitis, which are
CC applicable in foods, cosmetics and drugs. The present sequence is a honey
CC bee RJP.
XX
XX Sequence 544 AA;
SQ Query Match 100.0%; Score 49; DB 8; Length 544;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAVNHQRKSA 10
Db |||||
21 AAVNHQRKSA 30
RESULT 5
ABB64181
ID ABB64181 standard; protein; 347 AA.
XX
XX ABB64181;
XX 26-MAR-2002 (first entry)
DT Drosophila melanogaster polypeptide SEQ ID NO 19335.
DE Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
KW Drosophila melanogaster.
OS WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
PF 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
PA Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
DR N-PSDB; ABL07876.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX Disclosure; SEQ ID NO 18111; 21pp + Sequence Listing; English.
PS The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
DR N-PSDB; ABL08284.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX Disclosure; SEQ ID NO 19335; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 347 AA;
SQ Query Match 73.5%; Score 36; DB 4; Length 347;
Best Local Similarity 77.8%; Pred. No. 89;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAVNHQRKS 9
Db |||||
145 AAVNHQRQS 153
RESULT 6
ABB63773
ID ABB63773 standard; protein; 503 AA.
XX
XX ABB63773;
XX 26-MAR-2002 (first entry)
DT Drosophila melanogaster polypeptide SEQ ID NO 18111.
DE Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
KW Drosophila melanogaster.
OS WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
PF 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
PA Venter JC, Adams M, Li PWD, Myers EW;
PI WPI; 2001-656860/75.
DR N-PSDB; ABL07876.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX Disclosure; SEQ ID NO 18111; 21pp + Sequence Listing; English.
PS The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 503 AA;
Query Match 73.5%; Score 36; DB 4; Length 503;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 AVNHQKSA 10
Db 29 AVRHQRSA 37
|||
|
RESULT 7
ABG14172
ID ABG14172 standard; protein; 599 AA.
XX
AC ABG14172;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #14163.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS78359.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 44531; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABC0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 599 AA;
Query Match 73.5%; Score 36; DB 4; Length 599;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAVNHQK 8
Db 141 AAINHQK 148
|||
|
RESULT 8
AAU32811
ID AAU32811 standard; protein; 599 AA.
XX
AC AAU32811;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #3302.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US008656.
XX
PR 18-APR-2000; 2000US-00552929.
PR 26-JAN-2001; 2001US-00770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX
PS Claim 20; Page 668-669; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 599 AA;

Query Match 73.5%; Score 36; DB 4; Length 599;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVNHQK 8
||:||||:
Db 141 AAINHQK 148

RESULT 9
AAU40932
ID AAU40932 standard; protein; 535 AA.
XX AC AAU40932;
XX DT 13-FEB-2002 (first entry)
XX DE Propionibacterium acnes immunogenic protein #1828.
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX KW dermatological; osteopathic; neuroprotectant.
XX OS Propionibacterium acnes.
XX PN WO200181581-A2.
XX PD 01-NOV-2001.
XX PF 20-APR-2001; 2001WO-US012865.
XX PR 21-APR-2000; 2000US-0199047P.
XX PR 02-JUN-2000; 2000US-0208841P.
XX PR 07-JUL-2000; 2000US-0216747P.
XX XX (CORI-) CORIXA CORP.
XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX DR WPI; 2001-616774/71.
XX DR N-PSDB; AAS59513.
XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris.

Example 1; SEQ ID NO 2127; 1069pp; English.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 535 AA;

Query Match 71.4%; Score 35; DB 4; Length 535;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVNHQKSA 10
|||||:
Db 488 AAVNHSRTAA 497

RESULT 10
ABM37451
ID ABM37451 standard; protein; 535 AA.
XX AC ABM37451;
XX DT 20-OCT-2003 (first entry)
XX DE Propionibacterium acnes predicted ORF-encoded polypeptide #2127.
XX KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX KW immunostimulant; immune response; vaccine.
XX OS Propionibacterium acnes.
XX PN WO2003033515-A1.
XX PD 24-APR-2003.
XX PF 11-OCT-2002; 2002WO-US032727.
XX PR 15-OCT-2001; 2001US-00978825.
XX XX (CORI-) CORIXA CORP.
XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
XX PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
XX PI Barth B, Vallieue-Douglas J;
XX DR WPI; 2003-381789/36.
XX DR N-PSDB; ACF64442.
XX PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX PT or for stimulating an immune response specific for a P. acnes protein.
XX PS Example 1; SEQ ID NO 2127; 1481pp; English.

The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition comprising P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide; a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 535 AA;

Query Match 71.4%; Score 35; DB 6; Length 535;
 Best Local Similarity 70.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAVNHQKSA 10
 Db 488 AAVNHSRTAA 497
 ||||| :|

RESULT 11
 ADD31051
 ID ADD31051 standard; protein; 664 AA.

AC ADD31051;

DT 15-JAN-2004 (first entry)

XX Plant yield-related protein from clone G1079.

DE transcription factor; transgenic plant; growth rate; senescence;
 KW seed germination rate; plant vigor; seedling vigor.

XX Arabidopsis thaliana.

OS WO2003013227-A2.

PN 20-FEB-2003.

XX 09-AUG-2002; 2002WO-US025805.

XX 09-AUG-2001; 2001US-0310847P.

PR 19-NOV-2001; 2001US-0336049P.

PR 11-DEC-2001; 2001US-0338692P.

PR 14-JUN-2002; 2002US-00171468.

XX (MEND-) MENDEL BIOTECHNOLOGY INC.

XX Ratcliffe O, Riechmann JL, Adam LJ, Dubell AT, Heard JE;
 PI Pilgrim ML, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G;
 PI Broun PE;

XX WPI: 2003-248221/24.

DR N-PSDB; ADD31050.

XX New plant transcription factor polynucleotides and polypeptides, useful
 PT in producing transgenic plants with commercially valuable properties,
 PT such as an alteration in a plant growth characteristic, e.g. growth rate
 PT or apomixis.

PS Disclosure; SEQ ID NO 1080; 454pp; English.

XX The invention relates to a number of isolated Arabidopsis thaliana cDNA
 CC sequences and their encoded proteins which are especially transcription
 CC factor related cDNA's and proteins. The isolated or recombinant plant
 CC transcription factor polynucleotides and polypeptides are useful in
 CC producing transgenic plants with commercially valuable properties, i.e.
 CC modified or altered desirable traits as compared to a reference plant,
 CC such as an alteration in a plant growth characteristic, e.g. growth rate,
 CC germination rate of seeds, vigor of plants and seedlings, or leaf and
 CC flower senescence. Sequence information related to the polynucleotides
 CC and polypeptides can also be used in bioinformatic search methods. The
 CC transgenic plant is useful for growing a progeny plant from a parent
 CC plant. This sequence represents one of the proteins of the invention.

SQ Sequence 664 AA;

Query Match 71.4%; Score 35; DB 7; Length 664;
 Best Local Similarity 70.0%; Pred. No. 2.8e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAVNHQKSA 10
 Db 359 AKVEHERKSA 368
 ||||| :|

RESULT 12

ADI44067

ID ADI44067 standard; protein; 664 AA.

AC ADI44067;

DT 22-APR-2004 (first entry)

XX Plant transcription factor related polypeptide #1622.

XX transgenic; plant; enhanced tolerance to abiotic stress;
 KW phosphate tolerance; hormone sensitivity; disease resistance;
 KW sugar sensing; flowering; flower structure; stem bifurcation;
 KW branching pattern; apical dominance; trichome; stem morphology;
 KW root growth; root hair; seed development; cell proliferation;
 KW cell differentiation; premature senescence; necrosis; plant size;
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;
 KW transcription factor; ds.

XX Unidentified.

OS US2004019927-A1.

PN 29-JAN-2004.

XX 25-FEB-2003; 2003US-00374780.

XX 18-APR-2001; 2001US-00837944.

XX (SHER/) SHERMAN B K.

XX (RIEC/) RIECHMANN J L.

XX (JIANG/) JIANG C.

XX (HEAR/) HEARD J E.

XX (HAAK/) HAAKE V.

XX (CREE/) CREELMAN R A.

XX (RATC/) RATCLIFFE O.

XX (ADAM/) ADAM L J.

XX (REUB/) REUBER T L.

XX (KEDD/) KEDDIE J.

XX (BROU/) BROUN P E.

XX (PILG/) PILGRIM M L.

XX (DUBE/) DUBELL A N.

XX (PINE/) PINEDA O.

XX (YUGG/) YU G.

PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Haaake V;
 PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddle J, Broun PE;
 PI Pilgrim ML, Dubell AN, Pineda O, Yu G;

XX WPI: 2004-132245/13.

DR N-PSDB; ADI44066.

XX New transgenic plant comprising a recombinant polynucleotide of any one
 PT of more than 500 nucleotide sequences, useful in bioinformatic search
 PT methods.

PS Disclosure; SEQ ID NO 2530; 435pp; English.

XX The invention describes a transgenic plant comprising a recombinant
 CC polynucleotide of any one of more than 500 nucleotide sequences fully
 CC defined in the specification or its complement. The method of the
 CC invention can be used to produce a plant having altered traits such as:
 CC enhanced tolerance to abiotic stress; phosphate tolerance; hormone
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;
 CC altered flower structure, change in stem bifurcations, altered branching

CC pattern, reduced apical dominance, reduced trichome density; lack of
 CC trichomes; reduced ectopic trichome development; altered trichome
 CC development; increase in trichome number; altered stem morphology;
 CC increased root growth; increased root hairs; altered seed development;
 CC altered cell proliferation or cell differentiation; rapid development;
 CC premature senescence; increased necrosis; increase in seedling or plant
 CC size; decreased plant size; leaf morphology; seed morphology; seed
 CC biochemistry; increase in root anthocyanins; increase in plant
 CC anthocyanins; or alteration in light response or shade avoidance. The
 CC transgenic plant, polynucleotides and polypeptides are useful in
 CC bioinformatic search methods. This sequence represents a plant
 CC transcription factor related polynucleotide.

XX SQ Sequence 664 AA;

Query Match 71.4%; Score 35; DB 8; Length 664;
 Best Local Similarity 70.0%; Pred. No. 2.8e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAVNHQKSA 10
 Db 359 AKVEHERKSA 368

RESULT 13

ADN96832
 ID ADN96832 standard; protein; 5509 AA.

XX AC ADN96832;

DT 01-JUL-2004 (first entry)

XX Bugula bryostatin gene cluster ORF1 protein SeqID 43.

XX polyketide; bryopyran ring; bryostatin; polyketide synthase; PKS; toxic;
 KW cytosolic; immunomodulatory; protein therapy; cancer; metastasis.

XX Bugula.

XX WO2003099219-A2.

XX 04-DEC-2003.

XX 20-MAY-2003; 2003WO-US016299.

XX 20-MAY-2002; 2002US-0382181P.

XX (REGC) UNIV CALIFORNIA.

XX (HAYG/) HAYGOOD M.

XX (HILD/) HILDEBRAND M.

XX (ANDE/) ANDERSON C.

XX (WAGG/) WAGGONER L E.

XX (SHER/) SHERMAN D H.

XX (LIUH/) LIU H.

XX Haygood M, Hildebrand M, Anderson C, Waggoner LE, Sherman DH;
 PI Liu H;

XX WPI; 2004-053143/05.

XX New compositions comprising a polyketide synthase or nucleic acid
 PT encoding the polyketic synthase, useful in biosynthesizing polyketides,
 PT bryopyran rings and bryostatins having anti-cancer or antimetastatic
 PT activity.

XX Disclosure; Fig 25c; 342pp; English.

XX This invention relates to a novel composition that comprises at least one
 CC polypeptide that catalyses the one step synthesis of a polyketide or
 CC bryopyran ring. Specifically, it refers to nucleic acid molecules derived
 CC from marine organisms that encode enzymes that catalyse the synthesis of
 CC bioactive compounds such as polyketides and bryostatins that are based on
 CC the bryopyran ring structure. The present invention describes methods for

CC the use of polyketide synthases (PKSs) to generate toxic polyketides that
 CC exhibit cytostatic and immunomodulatory activities, such that they can be
 CC used for protein therapy in the treatment of cancer and metastasis. This
 CC polypeptide is a Bugula bryostatin biosynthetic gene cluster encoded
 CC protein of the invention. NOTE: This SeqID number is also attributed to a
 XX primer given in figure 28b.

XX SQ Sequence 5509 AA;

Query Match 71.4%; Score 35; DB 8; Length 5509;
 Best Local Similarity 66.7%; Pred. No. 2.6e+03;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVNHQKKS 9
 Db 3131 SAVNHQKKN 3139

RESULT 14

ADN96829
 ID ADN96829 standard; protein; 6940 AA.

XX AC ADN96829;

XX 01-JUL-2004 (first entry)

XX Bugula bryostatin gene cluster encoded protein (reading frame 2).

XX polyketide; bryopyran ring; bryostatin; polyketide synthase; PKS; toxic;
 KW cytosolic; immunomodulatory; protein therapy; cancer; metastasis.

XX Bugula.

XX Key Location/Qualifiers

FT Misc-difference 1. .6940

FT /label= Xaa

FT /note= "Xaa = in frame stop codons"

XX WO2003099219-A2.

XX 04-DEC-2003.

XX 20-MAY-2003; 2003WO-US016299.

XX 20-MAY-2002; 2002US-0382181P.

XX (REGC) UNIV CALIFORNIA.

XX (HAYG/) HAYGOOD M.

XX (HILD/) HILDEBRAND M.

XX (ANDE/) ANDERSON C.

XX (WAGG/) WAGGONER L E.

XX (SHER/) SHERMAN D H.

XX (LIUH/) LIU H.

XX Haygood M, Hildebrand M, Anderson C, Waggoner LE, Sherman DH;
 PI Liu H;

XX WPI; 2004-053143/05.

XX New compositions comprising a polyketide synthase or nucleic acid
 PT encoding the polyketic synthase, useful in biosynthesizing polyketides,
 PT bryopyran rings and bryostatins having anti-cancer or antimetastatic
 PT activity.

XX Disclosure; Fig 25a; 342pp; English.

XX This invention relates to a novel composition that comprises at least one
 CC polypeptide that catalyses the one step synthesis of a polyketide or
 CC bryopyran ring. Specifically, it refers to nucleic acid molecules derived
 CC from marine organisms that encode enzymes that catalyse the synthesis of
 CC bioactive compounds such as polyketides and bryostatins that are based on
 CC the bryopyran ring structure. The present invention describes methods for

CC the use of polyketide synthases (PKSs) to generate toxic polyketides that
 CC exhibit cytostatic and immunomodulatory activities, such that they can be
 CC used for protein therapy in the treatment of cancer and metastasis. This
 CC polypeptide is a Bugula bryostatins biosynthetic gene cluster encoded
 CC protein (reading frame 2) of the invention.

SQ Sequence 6940 AA;

Query Match 71.4%; Score 35; DB 8; Length 6940;

Best Local Similarity 66.7%; Pred. No. 3.4e+03;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVNHQRKS 9

:|||||:

Db 3321 SAVNHQKN 3329

RESULT 15

AD530840
 ID ADS30840 standard; protein; 284 AA.

XX AC

XX ADS30840;

XX DT

XX 02-DEC-2004 (first entry)

XX DE

XX Bacterial polypeptide #19873.

XX KW

Recombinant DNA construct; transformed plant; improved plant property;
 cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 pathogen tolerance; pest tolerance; plant disease resistance;
 cell cycle pathway modification; plant growth regulator;
 homologous recombination; seed oil yield; protein yield; carbohydrate;
 nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 bacterial polypeptide.

XX KW

XX OS

XX Bacteria.

XX XX

US2003233675-A1.

XX PN

XX 18-DEC-2003.

XX PD

20-FEB-2003; 2003US-00369493.

XX PF

21-FEB-2002; 2002US-0360039P.

XX PR

XX (CAOY/) CAO Y.

XX PA

XX (HINK/) HINKLE G J.

XX PA

XX (SLAT/) SLATER S C.

XX PA

XX (CHEN/) CHEN X.

XX PA

XX (GOLD/) GOLDMAN B S.

XX PI

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX DR

XX WPI; 2004-061375/06.

XX DR

New recombinant DNA construct comprising a promoter positioned to provide
 for expression of a polynucleotide encoding a polypeptide from a
 microbial source, useful for producing plants with improved properties.

XX PS

Claim 1; SEQ ID NO 19873; 122pp; English.

XX CC

The invention relates to a recombinant DNA construct comprising a
 promoter functional in a plant cell, where the promoter is positioned to
 provide for expression of a polynucleotide encoding a polypeptide from a
 microbial source. The invention also relates to a transformed plant
 comprising the recombinant DNA construct and a method of producing a
 transformed plant having an improved property. The plant is a crop plant
 such as maize or soybean. The method of producing a transformed plant
 having an improved property comprises transforming a plant with the
 recombinant DNA construct and growing the transformed plant, where the
 polynucleotide or polypeptide is useful for improving plant properties.
 The recombinant DNA construct is useful for producing plants with
 improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 284 AA;

Query Match 69.4%; Score 34; DB 8; Length 284;

Best Local Similarity 81.8%; Pred. No. 1.8e+02;

Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 AAVNH--QRKS 9

|||||

Db 126 AAVNHFKQRKS 136

Search completed: May 3, 2006, 19:01:23

Job time : 8.24897 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:01:48 ; Search time 0.751029 Seconds
(without alignments)
1281.133 Million cell updates/sec

Title: US-10-525-567-1
Perfect score: 49
Sequence: 1 AAVNHQKSA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	467	2 S39193	royal jelly protei
2	38	77.6	169	2 AF2630	hypothetical prote
3	37	75.5	194	2 B86073	hypothetical prote
4	37	75.5	194	2 D91226	Molybdopterin-guan
5	37	75.5	194	2 S40803	hypothetical prote
6	37	75.5	532	2 T49824	hypothetical prote
7	35	71.4	664	2 T01368	hypothetical prote
8	34	69.4	253	2 A88955	protein K04F1.1 [l
9	34	69.4	400	2 H69009	hypothetical prote
10	34	69.4	448	2 G87664	glycine cleavage s
11	34	69.4	479	2 S85466	xylose isomerase (
12	33	67.3	211	2 T47915	LIM domain protein
13	33	67.3	418	2 G87581	conjugal transfer
14	33	67.3	810	2 A81965	hemeoglobin-hapto
15	32	65.3	236	2 T45067	hypothetical prote
16	32	65.3	296	2 B81132	transcription regu
17	32	65.3	296	2 S24954	regulatory protein
18	32	65.3	305	2 A80863	positive regulator
19	32	65.3	305	2 F85932	glycine cleavage s
20	32	65.3	305	2 I41065	positive regulator
21	32	65.3	305	2 D91087	glycine cleavage s
22	32	65.3	305	2 AD0126	hypothetical prote
23	32	65.3	321	2 F82652	glycine betaine-bi
24	32	65.3	331	2 AC0842	adenosylhomocyste
25	32	65.3	527	1 S01302	phosphoprotein pho
26	32	65.3	692	1 PABY12	forked protein 5.6
27	32	65.3	1449	2 S57237	hypothetical prote
28	31	63.3	168	2 T17204	conserved hypothet
29	31	63.3	185	1 B69374	

30	31	63.3	275	2 A11965	hypothetical prote
31	31	63.3	433	2 T06407	monodehydroascorba
32	31	63.3	434	2 JU0182	monodehydroascorba
33	31	63.3	434	2 T47545	monodehydroascorba
34	31	63.3	470	2 S71355	glucocorticoid-att
35	31	63.3	472	2 A55508	interferon alpha I
36	31	63.3	524	2 T20872	hypothetical prote
37	31	63.3	626	2 I49100	macd6 precursor -
38	31	63.3	681	2 E64598	hypothetical prote
39	31	63.3	693	2 T19551	mucin-like protein
40	31	63.3	811	2 T39336	DEC1 protein homol
41	31	63.3	1024	2 AB0347	AcrtB/AcrtP/AcrtF fam
42	31	63.3	1047	2 T46489	hypothetical prote
43	31	63.3	1300	2 I53799	CGI protein - huma
44	31	63.3	1350	2 S00647	finger protein - A
45	31	63.3	1356	2 S32763	kinectin 1 - human

ALIGNMENTS

RESULT 1

S39193
royal jelly protein RJP57-1 - honeybee
C;Species: Apis mellifera (honeybee)
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 12-May-1995
C;Accession: S39193
R;Klaudiny, J.; Hanes, J.; Kulifajova, J.; Albert, S.; Simuth, J.
submitted to the EMBL Data Library, September 1993
A;Description: Molecular cloning of two cDNAs from the head of the nurse honey bee (Apis mellifera) encoding a protein that is highly homologous to the human kinectin 1.
A;Reference number: S39193
A;Accession: S39193
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-467 <KLA>
A;Cross-references: UNIPARC:UPI0000179A48; EMBL:Z26318

Query Match 100.0%; Score 49; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVNHQKSA 10
| | | | | | | | | |
Db 21 AAVNHQKSA 30

RESULT 2

AF2630
hypothetical protein Atu0441 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2630
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Wood, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, P.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, U.; E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2630
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <KUR>
A;Cross-references: UNIPROT:Q8UI59; UNIPARC:UPI000000D17ED; GB:AE008688; PIDN:AAL41460.1.
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0441
A;Map position: circular chromosome

Query Match 77.6%; Score 38; DB 2; Length 169;
Best Local Similarity 70.0%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAVNHQKSA 10
:|||||:|
Db 17 SAVNHGSRSA 26

RESULT 3

hypothetical protein mobA [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: B86073
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouzis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B86073
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-194 <STO>
A;Cross-references: UNIPARC:UPI00001659A4; GB:AE005174; NID:g12518733; PIDN:AAG59046.1;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: mobA
C;Superfamily: molybdopterin guanylyltransferase MobA

Query Match 75.5%; Score 37; DB 2; Length 194;
Best Local Similarity 70.0%; Pred. No. 2.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVNHQKSA 10
:|||||:|
Db 111 ARLNHQKDA 120

RESULT 4

D91226
Molybdopterin-guanine dinucleotide biosynthesis protein A [similarity] - Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C;Accession: D91226
R;Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D91226
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-194 <HAY>
A;Cross-references: UNIPROT:P58221; UNIPARC:UPI000012F34D; GB:BA000007; PIDN:BA038203.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EceA780
C;Superfamily: molybdopterin guanylyltransferase MobA

Query Match 75.5%; Score 37; DB 2; Length 194;
Best Local Similarity 70.0%; Pred. No. 2.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVNHQKSA 10
:|||||:|
Db 111 ARLNHQKDA 120

RESULT 5

S40803
molybdopterin-guanine dinucleotide biosynthesis protein A - Escherichia coli (strain K-12)
N;Alternate names: mob protein
C;Species: Escherichia coli
C;Date: 06-Oct-1994 #sequence_revision 26-May-1995 #text_change 05-Oct-2004
C;Accession: S40803; E65190

R;Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 21, 3391-3398, 1993
A;Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from 8;
A;Reference number: S40802; MUID:93347969; PMID:8346018

A;Accession: S40803

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-194 <PLU>

A;Cross-references: UNIPROT:P32173; UNIPARC:UPI0000111770; EMBL:L19201; NID:g304961; PIDN:

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: E65190

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-194 <BLAT>

A;Cross-references: UNIPARC:UPI0000111770; GB:AE0000461; GB:U00096; NID:g2367318; PIDN:AA0

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: mobA

A;Start codon: GTG

C;Superfamily: molybdopterin guanylyltransferase MobA

Query Match 75.5%; Score 37; DB 2; Length 194;
Best Local Similarity 70.0%; Pred. No. 2.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVNHQKSA 10
:|||||:|
Db 111 ARLNHQKDA 120

RESULT 6

T49824
hypothetical protein B24H17.100 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49824
R;Schulte, U.; Align, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49824
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-532 <SCH>
A;Cross-references: UNIPARC:UPI0000179E42; EMBL:AL356815; GSPDB:GN00116; NCSP:B24H17.100
A;Experimental source: BAC clone B24H17; strain OR74A
C;Genetics:
A;Gene: NCSP:B24H17.100
A;Map position: 6
A;Introns: 14/1; 169/1; 284/3; 429/1; 496/3

Query Match 75.5%; Score 37; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VNHQKS 9
:|||||
Db 221 VNHQKS 227

RESULT 7

T01368
hypothetical protein At2g34670 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T29F13.12
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01368; E84759
R;Roundley, S.D.; Lin, X.; Ketchum, K.A.; Croesby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, May 1998

A;Title: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
A;Reference number: Z14179
A;Accession: T01368
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-664 <ROU>
A;Cross-references: UNIPROT:O64589; UNIPARC:UPI00000A0612; EMBL:AC003096; NID:g3132469;
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84759
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-664 <STO>
A;Cross-references: UNIPARC:UPI00000A0612; GB:AE002093; NID:g3132478; PIDN:AAC16267.1; G
C;Genetics:
A;Gene: At2g34670; T29F13.12
A;Map position: 2
A;Introns: 294/1; 354/3; 429/2; 532/3
Query Match 71.4%; Score 35; DB 2; Length 664;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAVNHQRKSA 10
Db 359 AKVEHRKSA 368
RESULT 8
A88955
Protein K04F1.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A88955
R;Anonymous, The C. elegans Sequencing Consortium.
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: A88955
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <STO>
A;Cross-references: UNIPROT:Q9TXL6; UNIPARC:UPI000007C0A4; GB:chr_V; PIDN:AAC78175.1; PI
C;Genetics:
A;Gene: K04F1.1
A;Map position: 5
Query Match 69.4%; Score 34; DB 2; Length 253;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAVNHQRKSA 10
Db 3 AQINHVRKSS 12
RESULT 9
H69009
Hypothetical protein MTH1076 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69009
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwni, N.
k; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: H69009
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-400 <MTH>
A;Cross-references: UNIPROT:O27148; UNIPARC:UPI0000062B8B; GB:AE000879; GB:AE000666; NID
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1076
Query Match 69.4%; Score 34; DB 2; Length 400;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 3 VNHQRKSA 10
Db 182 VNHQRKSA 189
RESULT 10
G87664
glycine cleavage system P protein, subunit 1 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87664
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
n; J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87664
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <STO>
A;Cross-references: UNIPROT:Q9A353; UNIPARC:UPI000000C7A48; GB:AE005673; NID:g13425055; P
C;Genetics:
A;Gene: CC3353
C;Superfamily: Aquifex aeolicus glycine dehydrogenase (decarboxylating)
Query Match 69.4%; Score 34; DB 2; Length 448;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAVNHQRKSA 10
Db 352 AAVNHQRKSA 361
RESULT 11
S65466
xylose isomerase (EC 5.3.1.5) - barley
C;Species: Hordeum vulgare (barley)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65466; S65467; S65405
R;Kristo, P.; Saarelainen, R.; Fagerstroem, R.; Aho, S.; Korhola, M.
Eur. J. Biochem. 237, 240-246, 1996
A;Title: Protein purification, and cloning and characterization of the cDNA and gene for
A;Reference number: S65405; MUID:96203931; PMID:8620879
A;Accession: S65466
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-479 <KRI>
A;Cross-references: UNIPROT:Q40082; UNIPARC:UPI000016DDE9; EMBL:X95256; NID:g1296806; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
A;Accession: S65467
A;Molecule type: mRNA
A;Residues: 1-442; AGKGDETELEKKALENGEPTVPSGKQ; 472-479 <KRF>
A;Cross-references: UNIPARC:UPI00000176187; EMBL:X95257
A;Accession: S65405
A;Molecule type: protein
A;Residues: 54-62; 69-86; 97-108; 128-135; 193-204; 235-246; 300-307; 321-330; 371-379 <KRW>

```

A;Cross-references: UNIPARC:UPI0000176188; UNIPARC:UPI0000176189; UNIPARC:UPI000017618A;
18F; UNIPARC:UPI0000176190
C;Genetics:
A;Introns: 20/3; 57/3; 82/3; 126/1; 156/3; 173/3; 200/2; 218/3; 252/3; 270/1; 285/2; 304
C;Superfamily: xylose isomerase
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match      59.4%; Score 34; DB 2; Length 479;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAVNHQK 8
      |||||:|
Db      258 AAVNHKK 265

RESULT 12
T47915
LIM domain protein - Arabidopsis thaliana
N;Alternate names: protein T20K12.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004
C;Accession: T47915
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quest
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z24480
A;Status: preliminary
A;Accession: T47915
A;Molecule type: DNA
A;Residues: 1-211 <DEH>
A;Cross-references: UNIPROT:Q9W2E1; UNIPARC:UPI000009EDBC; EMBL:AL137898
A;Experimental source: cultivar Columbia; BAC clone T20K12
C;Genetics:
A;Map position: 3
A;Introns: 46/3; 80/1; 89/3
A;Note: T20K12.130
C;Superfamily: cysteine and glycine-rich protein; LIM metal-binding repeat homology

Query Match      67.3%; Score 33; DB 2; Length 211;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 AAVNHQKSA 10
      |||||:|
Db      173 AAANHRSTA 182

RESULT 13
G87581
conjugal transfer protein TrbI [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87581
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87581
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-418 <STO>
A;Cross-references: UNIPROT:Q9A4Y7; UNIPARC:UPI000000C77E7; GB:AB005673; NID:g13424269; F
C;Genetics:
A;Gene: CC2685

Query Match      67.3%; Score 33; DB 2; Length 418;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 AAVNHQK 8
      |||||:|

```

```

Db      114 AVINHQR 121

RESULT 14
A81965
hemeoglobin-haptoglobin-utilization protein NMA0474 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: A81965
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81965
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-810 <PAR>
A;Cross-references: UNIPROT:Q5JWA2; UNIPARC:UPI000012CB78; GB:AL162753; GB:AL157959; NID
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: hpuB; NMA0474

Query Match      67.3%; Score 33; DB 2; Length 810;
Best Local Similarity 77.8%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 AVNHQKSA 10
      |||||:|
Db      160 AVNYQTKSA 168

RESULT 15
T45067
hypothetical protein [imported] - Helicobacter pylori plasmid pHPM180
C;Species: Helicobacter pylori
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45067
R;Minnis, J.; Knesek, J.; Taylor, T.; McIntire, S.A.
submitted to the EMBL Data Library, July 1994
A;Description: Cloning and DNA sequence analysis of a plasmid from Helicobacter pylori.
A;Reference number: Z22904
A;Accession: T45067
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-236 <MIN>
A;Cross-references: UNIPROT:Q48249; UNIPARC:UPI00000B75FF; EMBL:U12689; PIDN:AAA20889.1
A;Experimental source: strain HPM180
C;Genetics:
A;Genome: plasmid pHPM180

Query Match      65.3%; Score 32; DB 2; Length 236;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 VNHQKSA 10
      |||||:|
Db      10 LNHERKNA 17

Search completed: May 3, 2006, 19:10:17
Job time : 2.75103 secs

```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 18:54:38 ; Search time 4.62963 Seconds

(without alignments)
1523.941 Million cell updates/sec

Title: US-10-525-567-1
Perfect score: 49
Sequence: 1 AAVNHORKSA 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	31	Q86R92 APIME	Q86R92 apis mellif
2	49	100.0	544	MRJP3 APIME	Q17060 apis mellif
3	40	81.6	344	Q7P382 FUSNY	Q7P382 fusobacteri
4	38	77.6	169	Q8UI59 AGRT5	Q8UI59 agrobacteri
5	37	75.5	194	MOBA_ECO57	P58221 escherichia
6	37	75.5	194	MOBA_ECOLI	P32173 escherichia
7	37	75.5	194	Q83P77 SHIFL	Q83P77 shigella fl
8	36	73.5	135	Q8BN36 MOUSE	Q8BN36 mus musculu
9	36	73.5	347	Q8BN36 MOUSE	Q97459 drosophila
10	36	73.5	347	Q9VXN1 DROME	Q9VXN1 drosophila
11	36	73.5	375	Q8SX00 DROME	Q8SX00 drosophila
12	36	73.5	503	Q9V7R7 DROME	Q9V7R7 drosophila
13	35	71.4	277	Q7NAK1 MYCGA	Q7NAK1 mycoplasma
14	35	71.4	304	Q4HFA2 CAMCO	Q4HFA2 campylobact
15	35	71.4	357	Q6MIG1 BDEBA	Q6MIG1 bdellovibri
16	35	71.4	369	Q6AJ53 DESPS	Q6AJ53 desulfotale
17	35	71.4	462	Q6ABV2 PROAC	Q6ABV2 propionibac
18	35	71.4	561	Q8GW98 ARATH	Q8GW98 arabidopsis
19	35	71.4	650	Q892X9 CLOTE	Q892X9 clostridium
20	35	71.4	664	Q64589 ARATH	Q64589 arabidopsis
21	35	71.4	689	Q8X179 EMENI	Q8X179 emericella
22	35	71.4	724	Q6FU10 CANGA	Q6FU10 candida gla
23	35	71.4	922	Q887R0 PSESM	Q887R0 pseudomonas
24	35	71.4	1307	Q7EWH0 NEUCR	Q7EWH0 neurospora
25	34	69.4	214	Q8FJ67_ECOL6	Q8FJ67 escherichia
26	34	69.4	244	Q9TXL6 CAEEL	Q9TXL6 caenorhabdi
27	34	69.4	284	Q5BQ55 EMENI	Q5BQ55 aspergillus
28	34	69.4	306	Q7N8R6 PHOLL	Q7N8R6 photorhabdu
29	34	69.4	354	Q5Q3W2 MACNE	Q5Q3W2 macaca neme
30	34	69.4	374	Q822Z0 CHLCV	Q822Z0 chlamydophi
31	34	69.4	387	Q9H5E5_HUMAN	Q9H5E5 homo sapien

Q76kc7 oryzias lat
Q90w00 oryzias lat
Q27148 methanobact
Q821g0 chlamydophi
Q4ip63 gibberella
Q53fw3 homo sapien
Q4ie78 gibberella
Q9a353 caulobacter
Q720w0 trypanosoma
Q40082 hordeum vul
Q6cz20 erwinia car
Q6zn44 homo sapien
Q4na44 arthrobacte
Q4pe10 ustilago ma

32 34 69.4 398 2 Q76KC7 ORYLA
33 34 69.4 398 2 Q90W00 ORYLA
34 34 69.4 400 2 Q27148 METHTH
35 34 69.4 410 2 Q821G0 CHLCV
36 34 69.4 412 2 Q4IP63 GIBZE
37 34 69.4 419 2 Q53FW3 HUMAN
38 34 69.4 431 2 Q4IE78 GIBZE
39 34 69.4 448 1 GCSPA CAUCR
40 34 69.4 452 1 Q720W0 TRYVI
41 34 69.4 479 1 XYLA HORVU
42 34 69.4 556 2 Q6CZ20 ERWCT
43 34 69.4 562 2 Q6ZN44 HOMAN
44 34 69.4 563 2 Q4NAF4 9MICC
45 34 69.4 1208 2 Q4PEL0 USTMA

ALIGNMENTS

RESULT 1

Q86R92 APIME
ID Q86R92 APIME PRELIMINARY; PRT; 31 AA.
AC Q86R92;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Major royal jelly protein MRJP3 (Fragment).
GN Name=MRJP3;
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22448659; PubMed=12559578; DOI=10.1016/S0378-1119(02)01174-5;
RA Malecova B., Ramser J., O'Brien J.K., Janitz M., Judova J.,
RA Lebrach H., Simuth J.;
RT "Honeybee (Apis mellifera L.) mrjp gene family: computational analysis
of putative promoters and genomic structure of mrjp1, the gene coding
for the most abundant protein of larval food.";
RL Gene 303:165-175(2003).
DR EMBL; AY078400; AAL83703.1; -; Genomic_DNA.
FT NON TER 31
SQ SEQUENCE 31 AA; 3371 MW; 566F7E355EDC627B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVNHORKSA 10
Db 21 AAVNHORKSA 30

RESULT 2

MRJP3 APIME
ID MRJP3 APIME STANDARD; PRT; 544 AA.
AC Q17060;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Major royal jelly protein 3 precursor (MRJP-3) (Bee-milk protein)
DE (Royal jelly protein RJP57-1).
GN Name=MRJP3;
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RT TISSUE=Head;

RA Klaudiny J., Hanes J., Kulifajova J., Albert S., Simuth J.;
RT "Molecular cloning of two cDNAs from the head of the nurse honey bee
RL (*Apis mellifera* L.) for coding related proteins of royal jelly."; J. Apicultural Res. 33:105-111(1994).
RN [2]
RP SEQUENCE REVISION TO THE C-TERMINUS.
RA Albert S., Klaudiny J., Simuth J.;
RT "Newly discovered features of the updated sequence of royal jelly
RT plectrin RJP571; longer repetitive region on C-terminus and homology to
RT *Drosophila melanogaster* yellow protein."; J. Apicultural Res. 35:63-68(1996).
RL [3]
RN [4]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 21-36.
RC TISSUE=Head;
RX MEDLINE=99007754; PubMed=9791542; DOI=10.1007/s000180050229;
RA Schmitzova J., Klaudiny J., Albert S., Schroeder W., Schreckengost W.,
RA Hanes J., Judova J., Simuth J.;
RT "A family of major royal jelly proteins of the honeybee *Apis mellifera*
RT L."; Cell. Mol. Life Sci. 54:1020-1030(1998).
RL [4]
RN NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE OF 45-59; 70-77;
RP 106-120; 214-224 AND 243-253.
RC TISSUE=Hypopharyngeal gland;
RX MEDLINE=98055707; PubMed=9395329;
RA Onashi K., Natori S., Kubo T.;
RT "Change in the mode of gene expression of the hypopharyngeal gland
RT cells with an age-dependent role change of the worker honeybee *Apis*
RT *mellifera* L."; Eur. J. Biochem. 249:797-802(1997).
RL [1]
CC -1- FUNCTION: May play an important role in honeybee nutrition. It is
CC found in the royal jelly which is the food of the queen honey bee
CC larva. The royal jelly determines the development of the young
CC larvae and is responsible for the high reproductive ability of the
CC honeybee queen.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Hypopharyngeal glands of nurse honey bees.
CC -1- DEVELOPMENTAL STAGE: Produced by the cephalic glandular system of
CC the nurse honey bee.
CC -1- SIMILARITY: Belongs to the major royal jelly protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Z6318; CAA81227.1; -; mRNA.
DR Ensembl; ENSGAPG00000007331; *Apis mellifera*.
DR InterPro; IPR003534; Royaljelly.
DR PANTHER; PTHR10009; Royaljelly; 1.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW Direct protein sequencing; Glycoprotein; Repeat; Signal.
FT SIGNAL
FT CHAIN 1 20
FT REPEAT 21 544 Major royal jelly protein 3.
FT REPEAT 424 428 1.
FT REPEAT 429 433 2.
FT REPEAT 434 438 3.
FT REPEAT 439 443 4.
FT REPEAT 444 448 5.
FT REPEAT 449 453 6.
FT REPEAT 454 458 7.
FT REPEAT 459 463 8.
FT REPEAT 464 468 9.
FT REPEAT 469 473 10.
FT REPEAT 474 478 11.
FT REPEAT 479 483 12.
FT REPEAT 484 488 13.
FT REPEAT 489 493 14.
FT REPEAT 494 498 15.
FT REPEAT 499 503 16.
FT REPEAT 504 508 17.

FT REPEAT 509 513 18.
FT REPEAT 514 518 19.
FT REPEAT 519 523 20.
FT REGION 424 523 20 X 5 AA tandem repeats of [NKR]-Q-N-
FT [AGD]-[DNG].
FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 544 AA; 61662 MW; 4C8FFFC8A2759F52 CRC64;
Query Match 100.0%; Score 49; DB 1; Length 544;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAVNHQKSA 10
Db 21 AAVNHQKSA 30
|||||
RESULT 3
Q7P382_FUSNV PRELIMINARY; PRT; 344 AA.
AC Q7P382;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical cytosolic protein.
GN Name=FN2194;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 49256;
RA Karpatrial V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haselkorn R., Overbeek R., Kyrtides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABF01000005; EAA25090.1; -; Genomic_DNA.
DR InterPro; IPR009362; DUF1016.
DR Pfam; PF06250; DUF1016; 1.
KW Hypothetical protein.
SQ SEQUENCE 344 AA; 40197 MW; B7117B1C125645D9 CRC64;
Query Match 81.6%; Score 40; DB 2; Length 344;
Best Local Similarity 87.5%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAVNHQK 8
Db 275 AAVNHQK 282
|||||
RESULT 4
Q8UI59_AGR75 PRELIMINARY; PRT; 169 AA.
AC Q8UI59;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Atu0441.
GN OrderedLocustNames=Atu0441;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Roue G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*
RT C58.";
RL Science 294:2317-2323(2001).
DR ENBL: AE009014; AAL41460.1; -; Genomic_DNA.
DR PIR: AP2630; AP2630.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 169 AA; 19428 MW; FDBBB0BACSD38EB CRC64;

Query Match 77.6%; Score 38; DB 2; Length 169;
Best Local Similarity 70.0%; Pred. No. 8.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAVNHQKSA 10
Db :|||||:
17 SAVNHSRRA 26

RESULT 5
MOBA_ECOLI
ID MOBA_ECOLI STANDARD; PRT; 194 AA.
AC P58221;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Molybdopterin-guanine dinucleotide biosynthesis protein A (Protein
DE FA).
GN Name=moba; Synonyms=chlB, mob, narB; OrderedLocusNames=z5389, ECs4780;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11208551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7";
RL Nature 409:529-533(2001).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN NUCLEOTIDE SEQUENCE OF 87-194.
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RA Ohnishi M., Murata T., Nakayama K., Kuhara S., Hattori M.,
RA Kurokawa K., Yasunaga T., Makino K., Shinagawa H., Hayashi T.;
RT "Development of primer sets for direct sequence determination of all
RT the ribosomal operons of *Escherichia coli*";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Links a guanosine 5'-phosphate to molybdopterin (MPT)
CC forming molybdopterin guanine dinucleotide (MGD) (By similarity).

CC -!- COFACTOR: Magnesium (By similarity).
CC -!- PATHWAY: Molybdenum cofactor biosynthesis.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the mobA family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC ENBL: AE005174; AAG59046.1; -; Genomic_DNA.
DR ENBL: BA000007; BAB38203.1; -; Genomic_DNA.
DR ENBL: AB035920; BAA93557.1; -; Genomic_DNA.
DR PIR: D91226; D91226.
DR HSSP: P32173; 1FR9.
DR HAMAP: MF_00316; -; 1.
DR Complete proteome; GTP-binding; Magnesium;
KW Molybdenum cofactor biosynthesis; Nucleotide-binding.
SQ SEQUENCE 194 AA; 21629 MW; E6F2ABDEC7BA2205 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 194;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAVNHQKSA 10
Db :|||||:
111 ARLNHQKDA 120

RESULT 6
MOBA_ECOLI
ID MOBA_ECOLI STANDARD; PRT; 194 AA.
AC P32173; Q9LBV0;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Molybdopterin-guanine dinucleotide biosynthesis protein A (Protein
DE FA).
GN Name=moba; Synonyms=chlB, mob, narB; OrderedLocusNames=b3857;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=K12 / MG1655;
RX MEDLINE=93347969; PubMed=8346018;
RA Plunkett G. III, Burland V., Daniels D.L., Blattner F.R.;
RT "Analysis of the *Escherichia coli* genome. III. DNA sequence of the
RT region from 87.2 to 89.2 minutes.";
RL Nucleic Acids Res. 21:3391-3398(1993).
RN NUCLEOTIDE SEQUENCE OF 1-5, AND CHARACTERIZATION.
RP STRAIN=K12;
RX MEDLINE=94291668; PubMed=8020507;
RA Palmer T., Vasiht A., Whitty P.W., Boxer D.H.;
RT "Isolation of protein FA, a product of the mob locus required for
RT molybdenum cofactor biosynthesis in *Escherichia coli*.";
RL Eur. J. Biochem. 222:687-692(1994).
RN CHARACTERIZATION.
RP STRAIN=K12;
RX MEDLINE=96004466; PubMed=7551035;
RA Iobbi-Nivol C., Palmer T., Whitty P.W., McNairn E., Boxer D.H.;
RT "The mob locus of *Escherichia coli* K12 required for molybdenum
RT cofactor biosynthesis is expressed at very low levels.";
RL Microbiology 141:1663-1671(1995).
RN X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RP MEDLINE=20568278; PubMed=10978347; DOI=10.1074/jbc.M007406200;
RX Lake M.W., Temple C.A., Rajagopalan K.V., Schindelin H.;

```

RT RT The crystal structure of the Escherichia coli Moba protein provides
RT insight into molybdopterin guanine dinucleotide biosynthesis.";
RL J. Biol. Chem. 275:40211-40217(2000).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).
RX PubMed=11080634; DOI=10.1016/S0969-2126(00)00518-9;
RA Stevenson C.E., Sargent F., Buchanan G., Falmer T., Lawson D.M.;
RT "Crystal structure of the molybdenum cofactor biosynthesis protein
RL Moba from Escherichia coli at near-atomic resolution.";
RL Structure 8:1115-1125(2000).
CC -i- FUNCTION: Links a guanosine 5'-phosphate to molybdopterin (MPT)
CC forming molybdopterin guanine dinucleotide (MGD).
CC -i- COFACTOR: Magnesium.
CC -i- PATHWAY: Molybdenum cofactor biosynthesis.
CC -i- SUBUNIT: Monomer.
CC -i- SUBCELLULAR LOCATION: Cytoplasmic.
CC -i- SIMILARITY: Belongs to the mobA family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; L19201; AAB02992.1; -; Genomic_DNA.
DR EMBL; U00096; AAC76855.1; -; Genomic_DNA.
DR PIR; S40803; S40803.
DR PDB; 1E5K; X-ray; A=1-194.
DR PDB; 1FR9; X-ray; A=1-194.
DR PDB; 1FRW; X-ray; A=1-194.
DR PDB; 1H4C; X-ray; A=1-194.
DR PDB; 1H4D; X-ray; A=1-194.
DR PDB; 1H4E; X-ray; A=1-194.
DR PDB; 1HJ1; X-ray; A=1-194.
DR PDB; 1HJL; X-ray; A=1-194.
DR EchoBASE; EB1776; -.
DR EcoGene; EGI1829; mobA.
DR HAMAP; MF 00316; -; 1.
DR 3D-structure; Complete proteome; Direct protein sequencing;
KW GTP-binding; Magnesium; Molybdenum cofactor biosynthesis;
KW Nucleotide-binding.
FT STRAND 7 12
FT HELIX 25 27
FT STRAND 29 30
FT TURN 31 32
FT STRAND 33 34
FT HELIX 35 46
FT STRAND 50 53
FT HELIX 58 62
FT TURN 63 64
FT STRAND 68 69
FT TURN 73 74
FT HELIX 79 89
FT STRAND 94 99
FT TURN 100 101
FT TURN 103 104
FT TURN 107 108
FT HELIX 109 115
FT TURN 116 116
FT TURN 118 119
FT STRAND 122 126
FT STRAND 131 139
FT TURN 140 141
FT HELIX 142 151
FT TURN 152 153
FT HELIX 157 163
FT TURN 164 165
FT STRAND 167 170
FT TURN 172 173
FT TURN 175 178
FT HELIX 184 188
FT TURN 189 190
SQ SEQUENCE 194 AA; 21643 MW; B79B32DD7348DD48 CRC64;

```

```

Query Match 75.5%; Score 37; DB 1; Length 194;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 AAVNHORKSA 10
Db 111 ARLNHORKDA 120

```

RESULT 7

```

Q83PF7_SHIFL
ID Q83PF7_SHIFL PRELIMINARY; PRT; 194 AA.
AC Q83PF7; Q7BZD5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Molybdopterin-guanine dinucleotide biosynthesis protein A.
GN Names-moba; OrderedLocustNames=S3819, SF3928;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RX DOI=10.1128/IAI.71.5.2775-2786.2003;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RA "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE005674; AAN45363.1; -; Genomic DNA.
DR EMBL; AE016990; AAP18835.1; -; Genomic_DNA.
DR HSSP; P32173; 1FR9.
DR SMR; Q83PF7; 4-191.
KW Complete proteome.
SQ SEQUENCE 194 AA; 21608 MW; 8933CCDECDDB46BE CRC64;

```

```

Query Match 75.5%; Score 37; DB 2; Length 194;
Best Local Similarity 70.0%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 AAVNHORKSA 10
Db 111 ARLNHORKDA 120

```

RESULT 8

```

Q8BN36_MOUSE
ID Q8BN36_MOUSE PRELIMINARY; PRT; 135 AA.
AC Q8BN36;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Mus musculus activated spleen cDNA, RIKEN full-length enriched
DE library, clone:F830008E12 product:hypothetical protein, full insert
DE sequence.

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RN Meth. Enzymol. 303:19-44(1999).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Bono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20493174; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20493174; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sui M., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multipillar sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD; TISSUE=Activated spleen;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tgami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AK089672; BAC40942.1; -; mRNA.
DR Ensembl; ENSMUSG0000063962; Mus musculus.
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 15774 MW; 5EP99816A8248EB CRC64;

Query Match 73.5%; Score 36; DB 2; Length 135;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVNHQRKS 9
DB 88 AVHQRKS 95
||:|||||
||:|||||

RESULT 9
O97459 DROME PRELIMINARY; PRT; 347 AA.
AC O97459
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE HCG-1.
GN Name=UBL3; Synonyms=HCG-1; ORFNames=CG9038;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99307157; PubMed=10375635; DOI=10.1016/S0378-1119(99)00138-9;
RA Chadwick B.P., Kidd T., Sgouros J., Ish-Horowitz D., Frischaut A.-M.;
RT "Cloning, mapping and expression of UBL3, a novel ubiquitin-like
gene.";
RL Gene 233:189-195(1999).
DR EMBL; AF044220; AAD02322.1; -; Genomic_DNA.
DR EMBL; AF044219; AAD02321.1; -; mRNA.
DR SMR; O97459; 231-335.
DR Ensembl; CG9038; Drosophila melanogaster.
DR FlyBase; FBgn0026076; CG9038.
DR FlyBase; FBgn0026076; UBL3.
DR GO; GO:0006464; P:protein modification; IEA.
DR InterPro; IPR000626; Ubiquitin.
DR PROSITE; PS0053; UBIQUITIN_2; 1.
SQ SEQUENCE 347 AA; 38086 MW; 5AC952F01D7AEFA7 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVNHQRKS 9
DB 145 AAVHQRKS 153
||:|||||
||:|||||

RESULT 10
Q9VXN1 DROME
ID Q9VXN1 DROME PRELIMINARY; PRT; 347 AA.
AC Q9VXN1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG9038-PA, isoform A (CG9038-pb, isoform b) (LD03728p).
GN Name=UBL3; ORFNames=CG9038;

OS Drosophila melanogaster (fruit fly)
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=2019606; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazie R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.P., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence."
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomes perspective."
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review."
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacieb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Berkley;
 RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacieb J.,
 RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -I- INTERACTION:
 CC Q9VSV3:CG4483; NBExp=1; IntAct=EBI-165186, EBI-176779;
 CC EMBL; AB003500; AAF48527.1; -; Genomic_DNA.
 CC EMBL; BT021420; AAX33568.1; -; mRNA.
 DR SNR; Q9VKN1; 231-335.
 DR IntAct; Q9VKN1; -;
 DR Ensembl; CG9038; Drosophila melanogaster.
 DR FlyBase; Fgn0026076; CG9038.
 DR FlyBase; Fgn0026076; UBL3.
 DR GO; GO:006464; P:protein modification; IEA.
 DR InterPro; IPR000626; Ubiquitin.
 DR PROSITE; PS50053; UBIQUITIN_2; 1.
 SQ SEQUENCE 347 AA; 38072 MW; AF9D07A71D7AEFA6 CRC64;
 Query Match 73.5%; Score 36; DB 2; Length 347;
 Best Local Similarity 77.8%; Pred. No. 52;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAVNHQKS 9
 DB 145 AAVHHQQS 153
 |||:||||:
 |||:||||:
 RESULT 11
 Q8SX00 DROME
 ID Q8SX00_DROME PRELIMINARY; PRT; 375 AA.
 AC Q8SX00;
 DT 01-JUN-2002 (T:EMBLrel. 21, Created)
 DT 01-JUN-2002 (T:EMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (T:EMBLrel. 22, Last annotation update)
 DE RH47633P.
 GN ORFNames=CG9311;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacieb J., Faragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY094927; AAM11280.1; -; mRNA.

03

```
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R(LOW);
RX MEDLINE=22830409; PubMed=12949158; DOI=10.1099/mic.0.26427-0;
RA Papazisi L., Gorton T.S., Kutish G., Markham P.F., Browning G.F.,
RA Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;
RT "The complete genome sequence of the avian pathogen Mycoplasma
RT gallisepticum strain R(LOW).";
RL Microbiology 149:2307-2316 (2003).
DR EMBL; AE016969; AAP56999.1; -; Genomic_DNA.
DR InterPro; IPR001611; LRR.
DR PRINTS; PR00019; LEURICHRPT.
KW Complete proteome; Leucine-rich repeat; Repeat.
SQ SEQUENCE 277 AA; 32757 MW; 9D52D025DBAC1BC5 CRC64;

Query Match 71.4%; Score 35; DB 2; Length 277;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AVNHQKSA 9
Db 204 AINHONKS 211
|:|||||

RESULT 14
Q4HFA2_CAMCO PRELIMINARY; PRT; 304 AA.
AC Q4HFA2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hemolysin, putative.
GN ORFNames=CC00183;
OS Campylobacter coli RM2228.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306254;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RM2228;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR EMBL; AAPL0100006; EAL56539.1; -; Genomic DNA.
SQ SEQUENCE 304 AA; 34186 MW; 9BB9B7315D26FE51 CRC64;

Query Match 71.4%; Score 35; DB 2; Length 304;
Best Local Similarity 77.8%; Pred. No. 74;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AVNHQKSA 10
Db 117 AKNHQKSA 125
|:|||||

RESULT 15
Q6MIG1_BDEBA
ID Q6MIG1_BDEBA PRELIMINARY; PRT; 357 AA.
AC Q6MIG1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE UDP-N-acetylglucosamine-N-acetylmuramyl-(Pentapeptide)
DE pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
DE (EC 2.4.1.227).
GN Name=murG; OrderedLocusNames=Bd3197;
```

```
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692 (2004).
DR EMBL; BX842654; CAE80952.1; -; Genomic DNA.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0030246; F:carbohydrate binding; IEA.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . . ; IEA.
DR GO; GO:0050511; F:undecaprenyldiphospho-muramoylpentapeptide . . . ; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0030259; P:lipid glycosylation; IEA.
DR GO; GO:0019277; P:UDP-N-acetylgalactosamine biosynthesis; IEA.
DR InterPro; IPR004276; Glyco_trans_28.
DR InterPro; IPR007235; Glyco_trans_28.
DR InterPro; IPR006009; MurG.
DR Pfam; PF03033; Glyco_transf_28; 1.
DR Pfam; PF04101; Glyco_tran_28_C; 1.
DR TIGRFAMs; TIGR01133; murG; 1.
DR TIGRFAMs; TIGR01133; murG; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 357 AA; 38880 MW; 64C993ACEA94D881 CRC64;

Query Match 71.4%; Score 35; DB 2; Length 357;
Best Local Similarity 70.0%; Pred. No. 88;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAVNHQKSA 10
Db 287 AADNHQKNA 296
|:|||||

Search completed: May 3, 2006, 19:08:58
Job time : 8.62963 secs
```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:09:24 ; Search time 1.08025 Seconds
(without alignments)
765.341 Million cell updates/sec

Title: US-10-525-567-1

Perfect score: 49

Sequence: 1 AAVNHQKSA 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	36	73.5	170 2	US-09-270-767-44218
2	36	73.5	423 2	US-09-270-767-41561
3	33	67.3	355 2	US-09-248-796A-14612
4	32	65.3	77 2	US-09-583-110-4552
5	32	65.3	242 2	US-09-902-540-13487
6	32	65.3	249 2	US-09-107-532A-6748
7	32	65.3	302 2	US-09-252-991A-28202
8	32	65.3	309 2	US-09-489-039A-9949
9	32	65.3	504 1	US-08-896-005-3
10	32	65.3	692 2	US-09-487-538B-274
11	31	63.3	26 1	US-08-620-151-28
12	31	63.3	38 2	US-09-774-639-254
13	31	63.3	68 2	US-09-248-796A-24682
14	31	63.3	108 2	US-09-489-039A-10310
15	31	63.3	185 2	US-09-949-016-8153
16	31	63.3	221 2	US-09-902-540-14900
17	31	63.3	361 2	US-09-252-991A-30237
18	31	63.3	365 2	US-09-252-991A-20893
19	31	63.3	407 2	US-09-252-991A-20503
20	31	63.3	419 2	US-09-902-540-16674
21	31	63.3	432 2	US-09-252-991A-23622
22	31	63.3	433 1	US-08-417-492-2
23	31	63.3	458 2	US-09-328-352-5083
24	31	63.3	467 2	US-09-489-039A-10022
25	31	63.3	569 2	US-09-902-540-11992
26	31	63.3	667 2	US-09-252-991A-32588
27	31	63.3	1307 2	US-09-949-016-7561

Sequence 3, Appli
Sequence 9675, Ap
Sequence 2735, Ap
Sequence 57778, A
Sequence 5507, Ap
Sequence 57842, A
Sequence 42540, A
Sequence 29151, A
Sequence 25020, A
Sequence 1648, Ap
Sequence 27, Appl
Sequence 40759, A
Sequence 55975, A
Sequence 8415, Ap
Sequence 22, Appl
Sequence 37, Appl
Sequence 34, Appl
Sequence 16697, A

28 31 63.3 2440 2 US-09-632-033B-3
29 31 63.3 2451 2 US-09-949-016-9675
30 30 61.2 65 2 US-09-107-433-2735
31 30 61.2 71 2 US-09-270-767-57778
32 30 61.2 137 2 US-09-134-000C-5507
33 30 61.2 162 2 US-09-270-767-57842
34 30 61.2 185 2 US-09-270-767-42540
35 30 61.2 202 2 US-09-252-991A-29151
36 30 61.2 225 2 US-09-252-991A-25020
37 30 61.2 221 2 US-09-605-703B-1648
38 30 61.2 276 1 US-07-952-817-27
39 30 61.2 359 2 US-09-270-767-40759
40 30 61.2 359 2 US-09-270-767-55975
41 30 61.2 481 2 US-09-489-039A-8415
42 30 61.2 483 2 US-08-369-822C-22
43 30 61.2 483 2 US-08-582-776C-37
44 30 61.2 483 2 US-08-434-831B-34
45 30 61.2 543 2 US-09-902-540-16697

ALIGNMENTS

RESULT 1

US-09-270-767-44218
; Sequence 44218, Application US/09270767
; Patent No. 6703491

GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44218
; LENGTH: 170

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-44218

Query Match 73.5%; Score 36; DB 2; Length 170;

Best Local Similarity 77.8%; Pred. No. 9.7;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAVNHQKRS 9

Db 74 AAVHHQKRS 82

RESULT 2

US-09-270-767-41561
; Sequence 41561, Application US/09270767
; Patent No. 6703491

GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41561
; LENGTH: 423

TYPE: PRT

ORGANISM: Drosophila melanogaster

FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-41561

Query Match 73.5%; Score 36; DB 2; Length 423;

Best Local Similarity 77.8%; Pred. No. 27;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 AAVNHQKRS 9
Db 221 AAVHHQKRS 229

RESULT 3
US-09-248-796A-14612
; Sequence 14612, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14612
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14612

Query Match 67.3%; Score 33; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NHQKRS 9
Db 279 NHQKRS 284

RESULT 4
US-09-583-110-4552
; Sequence 4552, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR FILING DATE: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4552
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4552

Query Match 65.3%; Score 32; DB 2; Length 77;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAVNHQKSA 10
Db 10 AALAHQRAA 19

RESULT 5
US-09-902-540-13487
; Sequence 13487, Application US/09902540
```

```
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13487
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13487

Query Match 65.3%; Score 32; DB 2; Length 242;
Best Local Similarity 75.0%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVNHQKRS 9
Db 23 AVDHQKRS 30

RESULT 6
US-09-107-532A-6748
; Sequence 6748, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6748:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
```

```

;
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...249
; SEQUENCE DESCRIPTION: SEQ ID NO: 6748:
US-09-107-532A-6748
Query Match 65.3%; Score 32; DB 2; Length 249;
Best Local Similarity 75.0%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Qy 2 AVNHQKRS 9
Db 157 AVNHPRKN 164
|||||

RESULT 7
US-09-252-991A-28202
; Sequence 28202, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28202
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28202
Query Match 65.3%; Score 32; DB 2; Length 302;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAVNHQKRS 9
Db 41 AAVSHQVKS 49
|||||

RESULT 8
US-09-489-039A-9949
; Sequence 9949, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9949
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9949
Query Match 65.3%; Score 32; DB 2; Length 309;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAVNHQKRS 9
Db 39 AAVSHQVKS 47
|||||

FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...249
SEQUENCE DESCRIPTION: SEQ ID NO: 6748:
US-09-107-532A-6748
Query Match 65.3%; Score 32; DB 2; Length 249;
Best Local Similarity 75.0%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Qy 2 AVNHQKRS 9
Db 157 AVNHPRKN 164
|||||

RESULT 9
US-08-896-005-3
; Sequence 3, Application US/08896005
; Patent No. 5854023
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,005
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0337 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 969078
US-08-896-005-3
Query Match 65.3%; Score 32; DB 1; Length 504;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NHQRKSA 10
Db 57 NHQRNSA 63
|||||

RESULT 10
US-09-487-558B-274
; Sequence 274, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
```

APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.130
CURRENT APPLICATION NUMBER: US/09/487,558B
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 446
SOFTWARE: PatentIn version 3.0
SEQ ID NO 274
LENGTH: 692
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-274

Query Match 65.3%; Score 32; DB 2; Length 692;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 VNHQKSA 10
| | | | |
DB 75 VNHQHS 82

RESULT 11
US-08-620-151-28
Sequence 28 Application US/08620151
Patent No. 5928955
GENERAL INFORMATION:
APPLICANT: Imperiali, Barbara
APPLICANT: Walkup, Grant K.
TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR
TITLE OF INVENTION: DIVERGENT ZINC
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,151
FILING DATE: 22-MAR-1996
CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
NAME: Shannon, Karen L.
REGISTRATION NUMBER: 36,675
REFERENCE/DOCKET NUMBER: 8597/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-620-151-28

Query Match 63.3%; Score 31; DB 1; Length 26;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 AAVNHQ 7
| | | | |
DB 16 ALVNHQ 22

RESULT 12
US-09-774-639-254
Sequence 254, Application US/09774639
Patent No. 6806351
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: PZ013P1
CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 371
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 254
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-774-639-254

Query Match 63.3%; Score 31; DB 2; Length 38;
Best Local Similarity 62.5%; Pred. No. 19;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VNHQKSA 10
: | : | | |
DB 1 IRHERKSA 8

RESULT 13
US-09-248-796A-24682
Sequence 24682, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 24682
LENGTH: 68
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-24682

Query Match 63.3%; Score 31; DB 2; Length 68;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AVNHQKSA 10
| | | | |
DB 35 APNHQKKA 43

RESULT 14
US-09-489-039A-10310
Sequence 10310, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

```
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10310
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10310

Query Match      63.3%; Score 31; DB 2; Length 108;
Best Local Similarity 70.0%; Pred. No. 61;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAVNHQKSA 10
      |||| :|||
Db      98 AAVNDERPSA 107

RESULT 15
US-09-949-016-8153
; Sequence 8153, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8153
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8153

Query Match      63.3%; Score 31; DB 2; Length 185;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 VNHQKSA 10
      :||| ||||
Db      68 LNHVRKSA 75

Search completed: May 3, 2006, 19:12:04
Job time : 2.08025 secs
```

end Page Blank (uspio)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:10:39 ; Search time 3.50823 Seconds
(without alignments)
1190.997 Million cell updates/sec

Title: US-10-525-567-1
Perfect score: 49
Sequence: 1 AAVNHQRKSA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap:*
5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap:*
6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	77.6	186	4	US-10-437-963-119181
2	36	73.5	347	6	US-11-097-143-19335
3	36	73.5	503	6	US-11-097-143-18111
4	36	73.5	599	5	US-10-450-763-44531
5	35	71.4	664	4	US-10-225-066A-1084
6	35	71.4	664	4	US-10-374-780A-2530
7	35	71.4	664	5	US-10-225-066A-1084
8	34	69.4	284	4	US-10-369-493-19873
9	34	69.4	291	5	US-10-450-763-38089
10	34	69.4	300	5	US-10-450-763-44774
11	34	69.4	445	5	US-10-450-763-35911
12	34	69.4	453	5	US-10-450-763-44530
13	34	69.4	454	5	US-10-450-763-36492
14	33	67.3	57	4	US-10-425-115-201509
15	33	67.3	108	4	US-10-425-115-253427
16	33	67.3	153	4	US-10-424-599-256805
17	33	67.3	250	4	US-10-282-122A-48895
18	33	67.3	291	5	US-10-450-763-38742
19	33	67.3	375	6	US-11-097-143-30918
20	33	67.3	1093	4	US-10-437-963-167806
21	33	67.3	3572	4	US-10-471-450-16
22	32	65.3	57	4	US-10-425-115-271519
23	32	65.3	58	4	US-10-425-115-287460
24	32	65.3	69	4	US-10-425-115-189718
25	32	65.3	71	5	US-10-450-763-33483
26	32	65.3	75	4	US-10-424-599-279595
27	32	65.3	83	5	US-10-450-763-56761

28	65.3	95	4	US-10-425-115-298869	Sequence 298869,
29	65.3	99	4	US-10-437-963-151148	Sequence 151148,
30	65.3	106	4	US-10-425-115-259425	Sequence 259425,
31	65.3	114	4	US-10-424-599-194647	Sequence 194647,
32	65.3	136	4	US-10-424-599-229751	Sequence 229751,
33	65.3	196	4	US-10-425-115-358696	Sequence 358696,
34	65.3	267	4	US-10-425-115-321509	Sequence 321509,
35	65.3	282	4	US-10-437-963-148332	Sequence 148332,
36	65.3	297	4	US-10-425-115-348894	Sequence 348894,
37	65.3	305	3	US-09-815-242-10277	Sequence 10277, A
38	65.3	305	3	US-09-815-242-13882	Sequence 13882, A
39	65.3	317	4	US-10-282-122A-71687	Sequence 71687, A
40	65.3	395	4	US-10-437-963-194504	Sequence 194504,
41	65.3	400	4	US-10-156-761-10393	Sequence 10393, A
42	65.3	425	4	US-10-425-114-54716	Sequence 54716, A
43	65.3	502	6	US-11-097-143-34098	Sequence 34098, A
44	65.3	504	6	US-11-097-143-41922	Sequence 41922, A
45	65.3	563	4	US-10-424-599-162116	Sequence 162116,

ALIGNMENTS

RESULT 1
US-10-437-963-119181
; Sequence 119181, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Bouharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 39-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 119181
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(186)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22422C.1.pap
US-10-437-963-119181

Query Match 77.6%; Score 38; DB 4; Length 186;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AAVNHQRKSA 10
| | | | | : | |
Db 160 AAVNHEQKKA 169

RESULT 2
US-11-097-143-19335
; Sequence 19335, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.

```

; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19335
; LENGTH: 347
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-19335

```

```

Query Match      73.5%; Score 36; DB 6; Length 347;
Best Local Similarity 77.8%; Pred. No. 87;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 AAVNHQKRS 9
Db      145 AAVHQRQS 153

```

RESULT 3

```

US-11-097-143-18111
; Sequence 18111, Application US/11097143
; Publication No. US2005020858A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18111
; LENGTH: 503
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-18111

```

```

Query Match      73.5%; Score 36; DB 6; Length 503;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 AAVNHQKSA 10
Db      29 AAVHQRSA 37

```

RESULT 4

```

US-10-450-763-44531
; Sequence 44531, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44531
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(599)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-44531

```

```

Query Match      73.5%; Score 36; DB 5; Length 599;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 AAVNHQK 8
Db      141 AAVNHQK 148

```

RESULT 5

```

US-10-225-066A-1084
; Sequence 1084, Application US/10225066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omalra
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI0036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049

```


; PRIOR FILING DATE: 2001-12-05
 ; PRIOR APPLICATION NUMBER: 60/338,692
 ; PRIOR FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: 10/171,468
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 1122
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1084
 ; LENGTH: 664
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-225-066A-1084

 Query Match 71.4%; Score 35; DB 4; Length 664;
 Best Local Similarity 70.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 1 AAVNHQKSA 10
 Db 359 AKVEHERKSA 368
 |||:||||

 RESULT 7
 US-10-225-066A-1084
 ; Sequence 1084, Application US/10225066A
 ; Publication No. US20050160493A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Mendel Biotechnology, Inc.
 ; APPLICANT: RATCLIFFE, Oliver
 ; APPLICANT: RIECHMANN, Jose Luis
 ; APPLICANT: ADAM, Luc J
 ; APPLICANT: DUBELL, Arnold T
 ; APPLICANT: HEARD, Jacqueline E
 ; APPLICANT: PILGRIM, Marsha L
 ; APPLICANT: JIANG, Cai-Zhong
 ; APPLICANT: REUBER, T. Lynne
 ; APPLICANT: CREELMAN, Robert A
 ; APPLICANT: PINEDA, Omaira
 ; APPLICANT: YU, Guo-Liang
 ; APPLICANT: BROWN, Pierre E
 ; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
 ; FILE REFERENCE: MBI0036-2 US
 ; CURRENT APPLICATION NUMBER: US/10/225,066A
 ; CURRENT FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 09/837,444
 ; PRIOR FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: 60/310,847
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 60/336,049
 ; PRIOR FILING DATE: 2001-12-05
 ; PRIOR APPLICATION NUMBER: 60/338,692
 ; PRIOR FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: 10/171,468
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 1122
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1084
 ; LENGTH: 664
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-225-066A-1084

 Query Match 71.4%; Score 35; DB 5; Length 664;
 Best Local Similarity 70.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 1 AAVNHQKSA 10
 Db 359 AKVEHERKSA 368
 |||:||||

 RESULT 8
 US-10-369-493-19873
 ; Sequence 19873, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493

; PRIOR FILING DATE: 2001-12-05
 ; PRIOR APPLICATION NUMBER: 60/338,692
 ; PRIOR FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: 10/171,468
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 1122
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1084
 ; LENGTH: 664
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-225-066A-1084

 Query Match 71.4%; Score 35; DB 4; Length 664;
 Best Local Similarity 70.0%; Pred. No. 2.7e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 1 AAVNHQKSA 10
 Db 359 AKVEHERKSA 368
 |||:||||

 RESULT 6
 US-10-374-780A-2530
 ; Sequence 2530, Application US/10374780A
 ; Publication No. US20040019927A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sherman, Bradley K
 ; APPLICANT: Riechmann, Jose Luis
 ; APPLICANT: Jiang, Cai-Zhong
 ; APPLICANT: Heard, Jacqueline E
 ; APPLICANT: Haake, Volker
 ; APPLICANT: Creelman, Robert A
 ; APPLICANT: Ratcliffe, Oliver
 ; APPLICANT: Adam, Luc J
 ; APPLICANT: Reuber, T. Lynne
 ; APPLICANT: Keddie, James
 ; APPLICANT: Brown, Pierre E
 ; APPLICANT: Pilgrim, Marsha L
 ; APPLICANT: Dubell III, Arnold T
 ; APPLICANT: Pineda, Omaira
 ; APPLICANT: Yu, Guo-Liang
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
 ; FILE REFERENCE: MBI-0047 CIP
 ; CURRENT APPLICATION NUMBER: US/10/374,780A
 ; CURRENT FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: 09/837,944
 ; PRIOR FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: 60/310,847
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 09/934,455
 ; PRIOR FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 60/336,049
 ; PRIOR FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/338,692
 ; PRIOR FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: 10/171,468
 ; PRIOR FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: 10/225,066
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/225,067
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/225,068
 ; PRIOR FILING DATE: 2002-08-09
 ; NUMBER OF SEQ ID NOS: 2906
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2530
 ; LENGTH: 664
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; OTHER INFORMATION: G1079
 ; US-10-374-780A-2530

```
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19873
; LENGTH: 284
; TYPE: PRT
; ORGANISM: No. US20030233675Altoc punctiforme
US-10-369-493-19873
```

```
Query Match          69.4%; Score 34; DB 4; Length 284;
Best Local Similarity 81.8%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
```

```
QY      1 AAVNH--QRKS 9
         ||||| |||||
Db       126 AAVNHFKQKKS 136
```

RESULT 9

```
US-10-450-763-38089
; Sequence 38089, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 38089
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
; NAME/KEY: DOMAIN
```

```
; LOCATION: (143)..(289)
```

```
; OTHER INFORMATION: Reverse transcriptase domain identified by PFam, accession
; OTHER INFORMATION: name rvt, E-value=5.8e-05, PFam score of 0.9
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (143)..(289)
; OTHER INFORMATION: Reverse transcriptase domain identified by PFam, accession
; OTHER INFORMATION: name rvt, E-value=9.135e-09, raw score of 11.58
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (240)..(252)
; OTHER INFORMATION: RNase H domain identified by eMATRIX, accession number
; OTHER INFORMATION: PF00075C, p-value=9.135e-09, raw score of 11.58
```

```
US-10-450-763-38089
```

```
Query Match          69.4%; Score 34; DB 5; Length 291;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAVNHQK 8
         ||:||||:
Db       66 AALNHQK 73
```

RESULT 10

```
US-10-450-763-44774
; Sequence 44774, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
```

```
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44774
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (228)..(244)
; OTHER INFORMATION: AUXIN BINDING PROTEIN SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00655E, p-value=7.222e-09, raw score of 8.06
US-10-450-763-44774
```

```
Query Match          69.4%; Score 34; DB 5; Length 300;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAVNHQK 8
         ||:||||:
Db       80 AALNHQK 87
```

RESULT 11

```
US-10-450-763-35911
; Sequence 35911, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 35911
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
; FEATURE:
```

```
; NAME/KEY: DOMAIN
```

```
; LOCATION: (6)..(36)
```

```
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354R, p-values=8.948e-17, raw score
; OTHER INFORMATION: 8.50
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (273)..(434)
; OTHER INFORMATION: Reverse transcriptase domain identified by PFam, accession
; OTHER INFORMATION: name rvt, E-value=4.9e-06, PFam score of 16.1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(445)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-35911
```

```
Query Match          69.4%; Score 34; DB 5; Length 445;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAVNHQK 8
         ||:||||:
Db       196 AALNHQK 203
```

RESULT 12
US-10-450-763-44530
; Sequence 44530, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44530
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (6)..(36)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354R, p-value=8.948e-17, raw score
; OTHER INFORMATION: 8.50
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(453)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-44530

Query Match 69.4%; Score 34; DB 5; Length 453;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVNHQK 8
DB 196 AALNHQK 203

RESULT 13
US-10-450-763-36492
; Sequence 36492, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 36492
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (6)..(36)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354R, p-value=8.948e-17, raw score
; OTHER INFORMATION: 8.50

US-10-450-763-36492

Query Match 69.4%; Score 34; DB 5; Length 454;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVNHQK 8
DB 196 AALNHQK 203

RESULT 14

US-10-425-115-201509
; Sequence 201509, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201509
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_11535C.1.pep
US-10-425-115-201509

Query Match 67.3%; Score 33; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHQKRS 9
DB 46 NHQKRS 51

RESULT 15

US-10-425-115-253427
; Sequence 253427, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 253427
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_162707C.1.pep
US-10-425-115-253427

Query Match 67.3%; Score 33; DB 4; Length 108;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NHQKSA 10
DB 60 NHQKSA 66

Search completed: May 3, 2006, 19:17:52
Job time : 5.50823 secs



GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:12:24 ; Search time 0.576132 Seconds
(without alignments)
803.371 Million cell updates/sec

Title: US-10-525-567-1

Perfect score: 49

Sequence: 1 AAVNHQKSA 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /SID55/ptodata/1/pubpaa/US08 NEW PUB.pep.1:
2: /SID55/ptodata/1/pubpaa/US06 NEW PUB.pep.*
3: /SID55/ptodata/1/pubpaa/US07 NEW PUB.pep.*
4: /SID55/ptodata/1/pubpaa/US08 NEW PUB.pep.*
5: /SID55/ptodata/1/pubpaa/PCT NEW PUB.pep.*
6: /SID55/ptodata/1/pubpaa/US09 NEW PUB.pep.*
7: /SID55/ptodata/1/pubpaa/US10 NEW PUB.pep.*
8: /SID55/ptodata/1/pubpaa/US10 NEW PUB.pep.*
9: /SID55/ptodata/1/pubpaa/US11 NEW PUB.pep.*
10: /SID55/ptodata/1/pubpaa/US11 NEW PUB.pep.*
11: /SID55/ptodata/1/pubpaa/US11 NEW PUB.pep.1:
12: /SID55/ptodata/1/pubpaa/US60 NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	67.3	284	11	US-11-079-463-5266
2	33	67.3	809	9	US-10-467-657-1106
3	33	67.3	810	11	US-11-052-554A-245
4	32	65.3	184	11	US-11-087-099-5689
5	32	65.3	297	11	US-11-096-568A-18592
6	32	65.3	432	11	US-11-087-099-8419
7	32	65.3	432	11	US-11-188-298-7797
8	32	65.3	599	11	US-11-087-099-1241
9	31	63.3	38	9	US-10-986-501-354
10	31	63.3	265	11	US-11-098-686-11404
11	30	61.2	133	9	US-10-467-657-5098
12	30	61.2	143	9	US-10-467-657-9090
13	30	61.2	237	9	US-10-714-887-254
14	30	61.2	267	11	US-11-188-298-3220
15	30	61.2	278	11	US-11-098-686-11365
16	30	61.2	341	9	US-10-515-481-12
17	30	61.2	341	11	US-11-087-099-1836
18	30	61.2	573	11	US-11-045-004-871
19	30	61.2	1159	9	US-10-055-877-139
20	30	61.2	1231	11	US-11-096-568A-28514
21	30	61.2	1253	11	US-11-096-568A-28513

ALIGNMENTS

RESULT 1

US-11-079-463-5266
Sequence 5266, Application US/11079463
Publication No. US20060073161A1

GENERAL INFORMATION:
APPLICANT: Gary L. Breton

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR

FILE REFERENCE: PATH00-03DIV2

CURRENT APPLICATION NUMBER: US/11/079,463

CURRENT FILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/128,705

PRIOR FILING DATE: 1999-04-09

PRIOR APPLICATION NUMBER: US 09/540,209

PRIOR FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 10444

SEQ ID NO 5266

LENGTH: 284

TYPE: PRT

ORGANISM: B.fragilis

US-11-079-463-5266

Query Match 67.3%; Score 33; DB 11; Length 284;
Best Local Similarity 87.5%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAVNHQK 8

Db 135 AAVNEQK 142

RESULT 2

US-10-467-657-1106

Sequence 1106, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: FONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

Sequence 28512, A
Sequence 8532, Ap
Sequence 4, Appl1
Sequence 17240, A
Sequence 393, App
Sequence 17239, A
Sequence 25, Appl1
Sequence 565, App
Sequence 11897, A
Sequence 10824, A
Sequence 6115, Ap
Sequence 17592, A
Sequence 10573, A
Sequence 4026, Ap
Sequence 2, Appl1
Sequence 13, Appl
Sequence 69, Appl
Sequence 10572, A
Sequence 9031, Ap
Sequence 8113, Ap
Sequence 10571, A
Sequence 19589, A
Sequence 2947, Ap
Sequence 638, App

11 US-11-096-568A-28512
9 US-10-467-657-8532
11 US-11-172-274-4
11 US-11-096-568A-17240
11 US-11-045-004-393
11 US-11-096-568A-17239
9 US-10-537-897-25
11 US-11-172-740-565
11 US-11-188-298-11897
11 US-11-096-568A-10824
11 US-11-188-298-6115
11 US-11-188-298-17592
11 US-11-096-568A-10573
9 US-10-467-657-4026
337 9 US-10-875-716-2
337 11 US-11-174-816-13
337 11 US-11-174-819-69
338 11 US-11-096-568A-10572
350 11 US-11-079-463-9031
351 11 US-11-188-298-8113
381 11 US-11-096-568A-10571
416 11 US-11-188-298-19589
441 8 US-10-511-937-2947
441 9 US-10-395-561-638

22 61.2 1401 11
23 59.2 76 9
24 59.2 92 11
25 59.2 236 11
26 59.2 252 11
27 59.2 254 11
28 59.2 261 9
29 59.2 261 11
30 59.2 261 11
31 59.2 302 11
32 59.2 309 11
33 59.2 331 11
34 59.2 332 9
35 59.2 337 9
36 59.2 337 11
37 59.2 337 11
38 59.2 338 11
39 59.2 350 11
40 59.2 351 11
41 59.2 381 11
42 59.2 416 11
43 59.2 441 8
44 59.2 441 9
45 59.2 441 9

```
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1106
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1106

Query Match      67.3%; Score 33; DB 9; Length 809;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AVNHQKSA 10
   |||:|
Db 160 AVNYQTKSA 168

RESULT 3
US-11-052-554A-245
; Sequence 245, Application US/11052554A
; Publication No. US20050289866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 245
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Neisseria meningitidis Z2491
US-11-052-554A-245

Query Match      67.3%; Score 33; DB 11; Length 810;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AVNHQKSA 10
   |||:|
Db 160 AVNYQTKSA 168

RESULT 4
US-11-087-099-5689
; Sequence 5689, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5689
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(184)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-5689

Query Match      65.3%; Score 32; DB 11; Length 184;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VNHQKSA 10
   |||:|
Db 166 VNHQKSA 173

RESULT 5
US-11-096-568A-18592
; Sequence 18592, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18592
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(297)
; OTHER INFORMATION: Ceres Seq. ID no. 12365991
US-11-096-568A-18592

Query Match      65.3%; Score 32; DB 11; Length 297;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAVNHQKRS 9
   |||:|
Db 230 AAQHQRKA 238

RESULT 6
US-11-087-099-8419
; Sequence 8419, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8419
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(432)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-8419

Query Match      65.3%; Score 32; DB 11; Length 432;
Best Local Similarity 75.0%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AVNHQKRS 9
   |||:|
Db 213 AVDHQRKS 220

RESULT 7
US-11-188-298-7797
; Sequence 7797, Application US/11188298
```

```

; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7797
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(432)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-188-298-7797

Query Match      65.3%; Score 32; DB 11; Length 432;
Best Local Similarity 75.0%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AVNHQKRS 9
Db      213 AVDHKRS 220
      ||:|||||

RESULT 8
US-11-087-099-1241
; Sequence 1241, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1241
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Coxiiella burnetii RSA 493
; US-11-087-099-1241

Query Match      65.3%; Score 32; DB 11; Length 599;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAVNHQKSA 10
Db      534 AAVNHQKSA 543
      ||:|||||

RESULT 9
US-10-986-501-354
; Sequence 354, Application US/10986501
; Publication No. US2005024845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06

; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7797
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(432)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-188-298-7797

Query Match      65.3%; Score 32; DB 11; Length 432;
Best Local Similarity 75.0%; Pred. No. 93;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AVNHQKRS 9
Db      213 AVDHKRS 220
      ||:|||||

RESULT 8
US-11-087-099-1241
; Sequence 1241, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1241
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Coxiiella burnetii RSA 493
; US-11-087-099-1241

Query Match      65.3%; Score 32; DB 11; Length 599;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAVNHQKSA 10
Db      534 AAVNHQKSA 543
      ||:|||||

RESULT 9
US-10-986-501-354
; Sequence 354, Application US/10986501
; Publication No. US2005024845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06

; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 7797
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(432)
; OTHER INFORMATION: unsure at all Xaa locations
US-11-188-298-7797

Query Match      65.3%; Score 31; DB 9; Length 38;
Best Local Similarity 62.5%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3 VNHQKSA 10
Db      1 IRHERKSA 8
      :|||

RESULT 10
US-11-098-686-11404
; Sequence 11404, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11404
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
; US-11-098-686-11404

Query Match      63.3%; Score 31; DB 11; Length 265;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AVNHQKSA 10
Db      103 AMNQKAA 111
      ||:|||||

RESULT 11
US-10-467-657-5098
; Sequence 5098, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

```

```
; FILE REFERENCE: MBI0058-CIP
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5098
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5098

Query Match      61.2%; Score 30; DB 9; Length 133;
Best Local Similarity 62.5%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VNHQKSA 10
Db 72 LNHQRPPA 79

RESULT 12
US-10-467-657-9090
; Sequence 9090, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9090
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9090

Query Match      61.2%; Score 30; DB 9; Length 143;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHQKSA 10
Db 45 NHQRQTA 51

RESULT 13
US-10-714-887-254
; Sequence 254, Application US/10714887
; Publication No. US20060015972A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: HEARD, Jacqueline
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: CREELMAN, Robert
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: CANALES, Roger
; APPLICANT: REPETTI, Peter
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal
; APPLICANT: REUBER, T. Lynne
; APPLICANT: PINEDA, Omalra
; APPLICANT: SHERMAN, Bradley K
; TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS

; FILE REFERENCE: MBI0058-CIP
; CURRENT APPLICATION NUMBER: US/10/714,887
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/135,134
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 254
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G3083 polypeptide; reference sequence
US-10-714-887-254

Query Match      61.2%; Score 30; DB 9; Length 237;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAVNHQKSA 10
Db 30 SAQNHHRNSA 39

RESULT 14
US-11-188-298-3220
; Sequence 3220, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 3220
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Oryza sativa (japonica cultivar-group)
US-11-188-298-3220

Query Match      61.2%; Score 30; DB 11; Length 267;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAVNHQKSA 10
Db 20 AAVHHNARSA 29

RESULT 15
US-11-098-686-11365
```


Thu May 4 17:23:15 2006

```
; Sequence 11365, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11365
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-11365
```

```
Query Match          61.2%; Score 30; DB 11; Length 278;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAVNHQKSA 10
      ||:||:||
Db      246 AAINHMDRTA 255
```

```
Search completed: May 3, 2006, 19:18:54
Job time : 1.57613 secs
```

This Page Blank (usp10)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 18:53:48 ; Search time 10.6224 Seconds
(without alignments)
1034.083 Million cell updates/sec

Title: US-10-525-567-2

Perfect score: 138

Sequence: 1 NLRGSLNKSUPILHEWKFDDYDF 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	25	8 ADL27605	Adl27605 Honey bee
2	138	100.0	413	8 ADL27607	Adl27607 Honey bee
3	138	100.0	414	8 ADL27617	Adl27617 Honey bee
4	138	100.0	432	4 AAG78710	Aag78710 Oxygen pr
5	138	100.0	432	4 AAG78815	Aag78815 Bee prote
6	138	100.0	432	8 ADL27619	Adl27619 Honey bee
7	101	73.2	25	4 AAG78709	Aag78709 Oxygen pr
8	101	73.2	25	4 AAG78814	Aag78814 Bee pepti
9	101	73.2	25	5 AAO20913	Aao20913 25-mer Ap
10	101	73.2	25	5 AAO14842	Aao14842 Honeybee
11	101	73.2	25	7 ADC52131	Adc52131 Apis mell
12	101	73.2	25	8 ADL06420	Adl06420 Protein-k
13	101	73.2	25	8 ADN61432	Adn61432 Honey bee
14	55.5	40.2	768	2 AA94918	Aaw94918 Rat phero
15	55	39.9	524	8 ADL27606	Adl27606 Honey bee
16	55	39.9	544	8 ADL27618	Adl27618 Honey bee
17	55	39.9	544	8 ADL27616	Adl27616 Honey bee
18	52	37.7	9	2 AAR28285	Aar28285 RJP9 - AC
19	52	37.7	42	4 ABB03089	Abb03089 Human mus
20	52	37.7	42	6 ABBU12383	Abu12383 Novel hum
21	52	37.7	42	6 ADJ28409	Adj28409 Human mus
22	51	37.0	281	6 ABM70854	Abm70854 Staphyloc
23	50	36.2	116	8 ADQ65186	Adq65186 Novel hum
24	49.5	35.9	255	6 ABUL6743	Abul6743 Protein e

25	49.5	35.9	270	8 ADP29330	Adp29330 Human sec
26	49.5	35.9	411	6 ADA33752	Ada33752 Acinetoba
27	49.5	35.9	610	6 ADA36517	Ada36517 Acinetoba
28	49.5	35.9	1029	6 ABR53179	Abr53179 Protein s
29	49.5	35.9	1029	7 ADK63210	Adk63210 Disease t
30	49	35.5	142	7 ADG30689	Adg30689 Xanthomon
31	49	35.5	768	5 ABB49385	Abb49385 Listeria
32	49	35.5	768	6 ABU32627	Abu32627 Protein e
33	48	34.8	400	8 ADN47954	Adn47954 Thermococ
34	48	34.8	445	8 ADX66511	Adx66511 Plant ful
35	48	34.8	904	5 ABP74080	Abp74080 Candida a
36	48	34.8	949	5 ABP35671	Abp35671 Fungal ZB
37	47.5	34.4	204	3 AAB08470	Aab08470 Amino aci
38	47	34.1	85	7 ADD25195	Add25195 Fertility
39	47	34.1	85	8 ADN61210	Adn61210 Radish nu
40	47	34.1	109	4 AAO00965	Aao00965 Human pol
41	47	34.1	242	8 ADX90871	Adx90871 Plant ful
42	47	34.1	242	8 ADX75685	Adx75685 Plant ful
43	47	34.1	380	4 AAU09147	Aau09147 Vasodilat
44	47	34.1	380	7 ADG46667	Adg46667 Human vas
45	47	34.1	380	8 ADJ14192	Adj14192 Human (va

ALIGNMENTS

RESULT 1

ADL27605
ID ADL27605 standard; peptide; 25 AA.

XX ADL27605;

XX 03-JUN-2004 (first entry)

DE Honey bee RJP55 N-terminal peptide, SEQ ID 2.

XX Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
royal jelly protein; allergy; pollinosis; atopic dermatitis;
contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP55.

OS Apis mellifera.

XX WO2004019971-A1.

XX 11-MAR-2004.

XX 26-AUG-2003; 2003WO-JP010795.

XX 29-AUG-2002; 2002JP-00252087.

XX 30-JAN-2003; 2003JP-00022776.

XX (HAYA/) HAYASHIBARA K.

XX Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;

XX WPI; 2004-248191/23.

XX Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,
atopic dermatitis, contact hypersensitivity, bronchial asthma and
allergic rhinitis, comprise protein originated from royal jelly.

XX Claim 2; SEQ ID NO 2; 78pp; Japanese.

XX The present invention relates to novel antiallergic agents, which
comprise as an active ingredient, peptides ADL27604 and ADL27605, which
are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606
and ADL27607). The agents can be used to relieve symptoms accompanying an
allergic disease e.g. pollinosis, atopic dermatitis, contact
hypersensitivity, bronchial asthma and allergic rhinitis, which are
applicable in foods, cosmetics and drugs.

XX Sequence 25 AA;

```

Query Match      100.0%; Score 138; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NILRGSLNKSLPILHEWKFFDYDF 25
   |||||
Db 1 NILRGSLNKSLPILHEWKFFDYDF 25

RESULT 2
ADL27607
ID ADL27607 standard; protein; 413 AA.
XX AC
XX AC ADL27607;
XX AC
DT 03-JUN-2004 (first entry)
XX AC
DE Honey bee RJP55 mature protein, SEQ ID 4.
XX AC
KW Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
KW royal jelly protein; allergy; pollinosis; atopic dermatitis;
KW contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP55.
XX OS
XX Apis mellifera.
XX WO2004019971-A1.
XX PN
XX PD 11-MAR-2004.
XX PF
XX PF 26-AUG-2003; 2003WO-JP010795.
XX PR
XX PR 29-AUG-2002; 2002JP-00252087.
XX PR 30-JAN-2003; 2003JP-00022776.
XX PR
XX PA (HAYA/) HAYASHIBARA K.
XX OKamoto I, Arai N, Kohno K, Kurimoto M, Sano O;
XX PI
XX PI WPI: 2004-248191/23.
XX DR
XX DR N-PSDB; ADL27609.
XX PT
XX PT Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,
XX PT atopic dermatitis, contact hypersensitivity, bronchial asthma and
XX PT allergic rhinitis, comprise protein originated from royal jelly.
XX PS
XX PS Disclosure; Page 62-65; 78pp; Japanese.
XX CC
XX CC The present invention relates to novel antiallergic agents, which
XX CC comprise as an active ingredient, peptides ADL27604 and ADL27605, which
XX CC are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606
XX CC and ADL27607). The agents can be used to relieve symptoms accompanying an
XX CC allergic disease e.g. pollinosis, atopic dermatitis, contact
XX CC hypersensitivity, bronchial asthma and allergic rhinitis, which are
XX CC applicable in foods, cosmetics and drugs. The present sequence is a honey
XX CC bee RJP.
XX SQ
XX SQ Sequence 414 AA;

Query Match      100.0%; Score 138; DB 8; Length 414;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NILRGSLNKSLPILHEWKFFDYDF 25
   |||||
Db 2 NILRGSLNKSLPILHEWKFFDYDF 26

RESULT 4
AAG78710
ID AAG78710 standard; protein; 432 AA.
XX AC
XX AC AAG78710;
XX AC
DT 11-DEC-2001 (first entry)
XX AC
DE Oxygen promoter related protein.
XX AC
KW Oxygen promoter; bee; royal jelly; cardiant; vulnerary;
KW cardiopulmonary function.
XX OS
XX OS Apis mellifera.
XX PN
XX PN JP2001172195-A.
XX PD
XX PD 26-JUN-2001.
XX PF
XX PF 15-DEC-1999; 99JP-00356005.
XX PF
XX PR 15-DEC-1999; 99JP-00356005.

```

```
XX PA (POKK ) POLA CHEM IND INC.
XX XX
XX DR WPI; 2001-592558/67.
XX DR N-PSDB; AAI64996.
XX PT Agent for promoting oxygen in cells to improve cardiopulmonary function,
XX PT comprises protein in royal jelly which comprises oxygen enhancing effect.
XX PS Disclosure; Page 9-10; 10pp; Japanese.
XX XX
XX CC The present invention relates to an agent for promoting oxygen,
XX CC comprising a protein in royal jelly which has an oxygen enhancing effect.
XX CC This can be used to promote oxygen in cells, causing an improvement in
XX CC pulmonary function. The present sequence is a protein which can be used
XX CC in the agent of the invention
XX XX
XX SQ Sequence 432 AA;
Query Match 100.0%; Score 138; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 9.4e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NILRGSLNKSPLILHEWKFFDYDF 25
Db 20 NILRGSLNKSPLILHEWKFFDYDF 44
RESULT 5
AAG78815
ID AAG78815 standard; protein; 432 AA.
XX AC
XX AC AAG78815;
XX XX
XX DT 27-NOV-2001 (first entry)
XX DE Bee protein.
XX KW Bee; lactic acid accumulation inhibitor; royal jelly; muscular fatigue.
XX OS Apis mellifera.
XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT Protein /label= Signal_peptide
XX FT Protein 20..432
XX FT Misc-difference 363
XX FT /label= Mature_bee_protein
XX FT /label= unknown
XX FT /note= "Encoded by CTN, given as Xaa in specification"
XX PN JP2001172190-A.
XX XX
XX PD 26-JUN-2001.
XX XX
XX PF 15-DEC-1999; 99JP-00356006.
XX PR 15-DEC-1999; 99JP-00356006.
XX XX
XX PA (POKK ) POLA CHEM IND INC.
XX XX
XX DR WPI; 2001-592556/67.
XX DR N-PSDB; AAI65041.
XX PT Lactic acid accumulation inhibitor comprises protein contained in royal
XX PT jelly, useful for restoration, improvement and release of muscular
XX PT fatigue.
XX PS Disclosure; Page 9-10; 10pp; Japanese.
XX XX
XX CC The present invention relates to a lactic acid accumulation inhibitor.
XX CC The inhibitor comprises a protein contained in royal jelly having lactic
XX CC acid accumulation inhibiting activity as the active component. The lactic
XX CC acid accumulation inhibitor is used for restoration, improvement and
XX CC release of muscular fatigue. The present sequence is a bee protein, which
XX CC was used in the present invention
XX SQ Sequence 432 AA;
Query Match 100.0%; Score 138; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 9.4e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NILRGSLNKSPLILHEWKFFDYDF 25
Db 20 NILRGSLNKSPLILHEWKFFDYDF 44
RESULT 6
ADL27619
ID ADL27619 standard; protein; 432 AA.
XX AC
XX AC ADL27619;
XX XX
XX DT 03-JUN-2004 (first entry)
XX DE Honey bee MRJP1.
XX KW Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
XX KW royal jelly protein; allergy; pollinosis; atopic dermatitis;
XX KW contact hypersensitivity; bronchial asthma; allergic rhinitis; MRJP1.
XX OS Apis mellifera.
XX FH Key Location/Qualifiers
XX FT Peptide 1..19
XX FT Protein /label= Signal_peptide
XX FT Protein 20..432
XX FT /label= Mature_protein
XX PN WO2004019971-A1.
XX PD 11-MAR-2004.
XX XX
XX PF 26-AUG-2003; 2003WO-JP010795.
XX PR 29-AUG-2002; 2002JP-00252087.
XX PR 30-JAN-2003; 2003JP-00022776.
XX XX
XX PA (HAYA/) HAYASHIBARA K.
XX XX
XX PI Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;
XX XX
XX DR WPI; 2004-248191/23.
XX DR N-PSDB; ADL27611.
XX XX
XX PT Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,
XX PT atopic dermatitis, contact hypersensitivity, bronchial asthma and
XX PT allergic rhinitis, comprise protein originated from royal jelly.
XX XX
XX PS Disclosure; Page 70-72; 78pp; Japanese.
XX XX
XX CC The present invention relates to novel antiallergic agents, which
XX CC comprise as an active ingredient, peptides ADL27604 and ADL27605, which
XX CC are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606
XX CC and ADL27607). The agents can be used to relieve symptoms accompanying an
XX CC allergic disease e.g. pollinosis, atopic dermatitis, contact
XX CC hypersensitivity, bronchial asthma and allergic rhinitis, which are
XX CC applicable in foods, cosmetics and drugs. The present sequence is a honey
XX CC bee major RJP.
XX SQ Sequence 432 AA;
Query Match 100.0%; Score 138; DB 8; Length 432;
Best Local Similarity 100.0%; Pred. No. 9.4e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 NILRGESLNKSLPILHEWKFFDYDF 25
Db      20 NILRGESLNKSLPILHEWKFFDYDF 44

RESULT 7
AAG78709
ID      AAG78709 standard; peptide; 25 AA.
XX
AC      AAG78709;
XX
DT      11-DEC-2001 (first entry)
XX
DE      Oxygen promoter related peptide.
XX
KW      Oxygen promoter; bee; royal jelly; cardiant; vulnery;
KW      cardiopulmonary function.
XX
OS      Apis mellifera.
XX
PN      JP2001172195-A.
XX
PD      26-JUN-2001.
XX
PF      15-DEC-1999; 99JP-00356005.
XX
PR      15-DEC-1999; 99JP-00356005.
XX
PA      (POKK ) POLA CHEM IND INC.
XX
WPI; 2001-592558/67.
XX
Lactic acid accumulation inhibitor comprises protein contained in royal
jelly, useful for restoration, improvement and release of muscular
fatigue.
XX
Claim 4; Page 7; 10pp; Japanese.
XX
The present invention relates to a lactic acid accumulation inhibitor.
The inhibitor comprises a protein contained in royal jelly having lactic
acid accumulation inhibiting activity as the active component. The lactic
acid accumulation inhibitor is used for restoration, improvement and
release of muscular fatigue. The present sequence is a bee peptide, which
was used in the present invention
XX
SQ      Sequence 25 AA;

Query Match      73.2%; Score 101; DB 4; Length 25;
Best Local Similarity 87.0%; Pred. No. 2.4e-08;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 NILRGESLNKSLPILHEWKFFDY 23
Db      1 NILRGESLNKSLPILHEWKFFDY 23

RESULT 9
AAO20913
ID      AAO20913 standard; peptide; 25 AA.
XX
AC      AAO20913;
XX
DT      08-JUL-2002 (first entry)
XX
DE      25-mer Apis mellifera peptide.
XX
KW      Antiapoptotic; hepatotropic; apoptosis inhibitor; royal jelly.
XX
OS      Apis mellifera.
XX
FH      Key      Location/Qualifiers
FT      Misc-difference 24
FT      /label= unknown
XX
PN      JP2002080391-A.
XX
PD      19-MAR-2002.
XX
PF      04-SEP-2000; 2000JP-00266421.
XX
PR      04-SEP-2000; 2000JP-00266421.
XX
PA      (POKK ) POLA CHEM IND INC.
XX
WPI; 2002-357223/39.
XX
An apoptosis inhibitor and a composition for hepatitis containing it.
XX
Claim 1; Page 5; 6pp; Japanese.
XX
The invention relates to an apoptosis inhibitor consisting of a protein
contained in royal jelly. It forms a single band in an unmodified
polyacrylamide gel electrophoresis of the protein in royal jelly. Its

QY      1 NILRGESLNKSLPILHEWKFFDY 23
Db      1 NILRGESLNKSLPILHEWKFFDY 23

RESULT 8
AAG78814
ID      AAG78814 standard; peptide; 25 AA.
XX
AC      AAG78814;
XX
DT      27-NOV-2001 (first entry)
XX
DE      Bee peptide.
XX
KW      Bee; lactic acid accumulation inhibitor; royal jelly; muscular fatigue.
XX
OS      Apis mellifera.
XX
FH      Key      Location/Qualifiers
FT      Misc-difference 24
FT      /note= "Unspecified residue"
XX

```

XX	ADC52131;
XX	18-DEC-2003 (first entry)
XX	Apis mellifera peptide SEQ ID NO 1.
XX	Protein-kinase B; glycoprotein; royal jelly; liver;
KW	congenital urea-cycle enzyme deficiency; hepatitis; alcoholic cirrhosis;
KW	Apis mellifera; hepatotropic; antialcoholic; virucide; antiinflammatory;
KW	Protein-kinase-stimulator-B; honeybee.
XX	Apis mellifera.
OS	
XX	Key Location/Qualifiers
FF	Misc-difference 24 /note= "Xaa = unknown"
FT	
XX	JP2003061648-A.
PN	
XX	04-MAR-2003.
PD	
XX	29-AUG-2001; 2001JP-00259187.
XX	
XX	29-AUG-2001; 2001JP-00259187.
PR	(POKK) POLA CHEM IND INC.
PA	
XX	WPI; 2003-580861/55.
XX	
PT	Protein-kinase B activator for use in pharmaceutical or foodstuffs for
PT	improving and recovering abnormal liver function and hepatitis, comprises
PT	a glycoprotein obtained from royal jelly.
XX	
PS	Disclosure; SEQ ID NO 1; 6pp; Japanese.
CC	The invention relates to a protein-kinase B activator, consisting of a
CC	glycoprotein obtained from royal jelly. The protein-kinase B activator is
CC	used in a composition such as pharmaceutical or foodstuffs for improving
CC	and recovering the abnormality of a liver function, congenital urea-cycle
CC	enzyme deficiency, acute hepatitis, chronic-hepatitis, alcoholic fatty
CC	liver, alcoholic cirrhosis, etc. The present sequence is that of an Apis
CC	mellifera (honeybee) peptide disclosed as part of the invention.
XX	
SQ	Sequence 25 AA;
	Query Match 73.2%; Score 101; DB 7; Length 25;
	Best Local Similarity 87.0%; Pred. No. 2.4e-08;
	Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 NTLRGESLNKSLPILHEWKFPDY 23
Db	1 NTLRGESLLKLLPILHEMKFPDY 23
RESULT 12	
ADL06420	ID ADL06420 standard; peptide; 25 AA.
XX	
AC	ADL06420;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Protein-kinase C activator associated Apis mellifera peptide.
XX	
KW	Protein-kinase C activator; glycoprotein; royal jelly;
KW	Protein-kinase activation; foodstuff; myocardial infarction;
XW	peroxide damage; cardiac; blood vessel; cardiant.
XX	
OS	Apis mellifera.
XX	
XX	Key Location/Qualifiers
FT	Misc-difference 24

XX SQ Sequence 768 AA;
Query Match 40.2%; Score 55.5; DB 2; Length 768;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 11; Conservative 2; Mismatches 6; Indels 3; Gaps 1;
Qy 3 LRGESLNSLPILHEWKFFDYD 24
Db 259 LRSRLNLLIP--EWKYFSYD 277
RESULT 15
ADL27606
ID ADL27606 standard; protein; 524 AA.
XX
XX AC ADL27606;
XX
XX DT 03-JUN-2004 (first entry)
XX DE Honey bee RJP70 mature protein, SEQ ID 3.
XX KW Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
KW royal jelly protein; allergy; pollinosis; atopic dermatitis;
KW contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP70.
XX OS Apis mellifera.
XX PN WO2004019971-A1.
XX PD 11-MAR-2004.
XX PF 26-AUG-2003; 2003WO-JP010795.
XX PR 29-AUG-2002; 2002JP-00252087.
XX PR 30-JAN-2003; 2003JP-00022776.
XX PA (HAYA/) HAYASHIBARA K.
XX FI Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;
XX DR WPI; 2004-248191/23.
XX DR N-PSDB; ADL27608.
XX PT Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,
PT atopic dermatitis, contact hypersensitivity, bronchial asthma and
PT allergic rhinitis, comprise protein originated from royal jelly.
XX PS Claim 1; SEQ ID NO 3; 78pp; Japanese.
XX CC The present invention relates to novel antiallergic agents, which
CC comprise as an active ingredient, peptides ADL27604 and ADL27605, which
CC are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606
CC and ADL27607). The agents can be used to relieve symptoms accompanying an
CC allergic disease e.g. pollinosis, atopic dermatitis, contact
CC hypersensitivity, bronchial asthma and allergic rhinitis, which are
CC applicable in foods, cosmetics and drugs.
XX SQ Sequence 524 AA;
Query Match 39.9%; Score 55; DB 8; Length 524;
Best Local Similarity 42.1%; Pred. No. 11;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
Qy 7 SLNKSILPILHEWKFFDYD 25
Db 12 NLAHMKVIYEWKHIDFDF 30
Search completed: May 3, 2006, 19:01:25
Job time : 12.6224 secs

The Page Block (upside)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:01:48 ; Search time 1.87757 Seconds
(without alignments)
1281.133 Million cell updates/sec

Title: US-10-525-567-2

Sequence: 1 NLRGESLNKSLPILHEWKFFDYDF 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: Piri.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	52.9	464	2 S39194	royal jelly protei
2	55	39.9	467	2 S39193	royal jelly protei
3	53	38.4	404	2 H88650	protein C09G12.9 l
4	50.5	36.6	869	2 S49844	probable membrane
5	50.5	36.6	1115	2 T11614	probable poly(A)-s
6	50	36.2	546	2 A80088	probable flagellar
7	50	36.2	809	2 T41645	probable spindle p
8	49.5	35.9	161	2 G83914	hypothetical prote
9	49.5	35.9	1029	2 S57598	PP5 protein - yea
10	49	35.5	160	2 T15925	hypothetical prote
11	49	35.5	445	2 B83743	N-ethylamine ch
12	49	35.5	768	2 A11085	hypothetical prote
13	48	34.8	384	2 S51796	vasodilator-stimul
14	48	34.8	949	2 S54020	probable membrane
15	47	34.1	380	2 S51797	vasodilator-stimul
16	47	34.1	627	2 S53369	carnitine O-acetyl
17	46.5	33.7	357	2 F70193	hypothetical prote
18	46.5	33.7	439	2 T45798	hypothetical prote
19	46	33.3	271	2 H97230	alpha/beta superfa
20	46	33.3	327	2 F84610	hypothetical prote
21	46	33.3	393	2 JC5614	RNB6 protein - rat
22	46	33.3	526	2 A75581	flavin monooamine o
23	46	33.3	634	2 T27881	hypothetical prote
24	46	33.3	671	2 A30746	chemotaxis protein
25	46	33.3	671	2 A38959	chemotaxis protein
26	46	33.3	705	2 A86497	conserved hypothet
27	46	33.3	705	2 F72125	conserved hypothet
28	46	33.3	1021	2 T08601	hypothetical prote
29	46	33.3	1026	2 C97783	cell surface anti

30	45.5	33.0	553	2 I40807	cellulase (EC 3.2.
31	45.5	33.0	636	2 JCS874	cellulase (EC 3.2.
32	45	32.6	67	2 AC1954	hypothetical prote
33	45	32.6	166	2 A48465	ribosomal protein
34	45	32.6	256	2 H72349	conserved hypothet
35	45	32.6	425	2 E86737	malate transporter
36	45	32.6	425	1 B40576	cytochrome P450 AL
37	45	32.6	538	1 O4CKA4	cytochrome P450 52
38	45	32.6	582	2 T39931	probable transcrip
39	45	32.6	627	2 D71974	hypothetical prote
40	45	32.6	628	2 B64534	hypothetical prote
41	45	32.6	772	2 T26313	hypothetical prote
42	44.5	32.2	473	2 T32038	hypothetical prote
43	44	31.9	139	2 A87442	Mut7/nudix family
44	44	31.9	219	2 JQ1606	multiple stimulus
45	44	31.9	240	2 H69846	hypothetical prote

ALIGNMENTS

RESULT 1

S39194

royal jelly protein RJP57-2 - honeybee

C;Species: Apis mellifera (honeybee)

C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004

C;Accession: S39194

R;Klaudiny, J.; Hanes, J.; Kulifajova, J.; Albert, S.; Simuth, J.

submitted to the EMBL Data Library, September 1993

A;Description: Molecular cloning of two cDNAs from the head of the nurse honey bee (Apis

A;Reference number: S39193

A;Accession: S39194

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-464 <KLA>

A;Cross-references: UNIPROT:Q17061; UNIPARC:UPI000012F56A; EMBL:Z26319; NID:G4333530; PID

Query Match 52.9%; Score 73; DB 2; Length 464;

Best Local Similarity 47.6%; Pred. No. 0.004;

Matches 10; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GESLNKSLPILHEWKFFDYDF 25

|||

Db 29 GKLTNTLNVTHKWKLYDYDF 49

RESULT 2

S39193

royal jelly protein RJP57-1 - honeybee

C;Species: Apis mellifera (honeybee)

C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 12-May-1995

C;Accession: S39193

R;Klaudiny, J.; Hanes, J.; Kulifajova, J.; Albert, S.; Simuth, J.

submitted to the EMBL Data Library, September 1993

A;Description: Molecular cloning of two cDNAs from the head of the nurse honey bee (Apis

A;Reference number: S39193

A;Accession: S39193

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-467 <KLA>

A;Cross-references: UNIPARC:UPI0000179A48; EMBL:Z26318

Query Match 39.9%; Score 55; DB 2; Length 467;

Best Local Similarity 42.1%; Pred. No. 2.2;

Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 7 SLNKSPLILHEWKFFDYDF 25

|||

Db 32 NLAHMKVIYEWKIDDF 50

RESULT 3

H88650

A;Cross-references: UNIPARC:UPI000006B647; EMBL:Z50111; NID:g914872; PID:g914873
A;Experimental source: strain AB972
C;Genetics:
A;Cross-references: SGD:S0002496
A;Map position: 4R
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YDR089W
C;Keywords: transmembrane protein
F;777-793/Domain: transmembrane #status predicted <TM1>
F;811-827/Domain: transmembrane #status predicted <TM2>
F;828-844/Domain: transmembrane #status predicted <TM3>

Query Match 36.6%; Score 50.5; DB 2; Length 869;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 9; Conservative 5; Mismatches 1; Indels 3; Gaps 1;

QY 8 LNKSLPILHWEKFPDYDF 25
||||| ||||| : :
Db 8 LNKSIPI---EWKFFNYNY 22
||||| ||||| : :

RESULT 5
Tl1614
probable poly(A)-specific ribonuclease (EC 3.1.13.4) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: Tl1614; S62448
R;Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z17300
A;Accession: Tl1614
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1115 <BAR>
A;Cross-references: UNIPROT:Q09798; UNIPARC:UPI0000139FED; EMBL:Z54328; NID:g1009451; PID:g1009451; P
A;Experimental source: strain 972h(-)
R;Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, October 1995
A;Reference number: S62445
A;Accession: S62448
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1115 <BAR>
A;Cross-references: UNIPARC:UPI0000139FED; EMBL:Z54328; NID:g1009451; PIDN:CAA91128.1; P
C;Genetics:
A;Map position: IL
A;Introns: 6/3; 39/3; 95/2; 164/3; 357/2; 793/1
A;Note: SPAC22G7.04
C;Keywords: hydrolase

Query Match 36.6%; Score 50.5; DB 2; Length 1115;
Best Local Similarity 39.3%; Pred. No. 30;
Matches 11; Conservative 5; Mismatches 7; Indels 5; Gaps 1;

QY 1 NILRGESLNKSLPILHEW-----KFPDY 23
:||||| ||||| : :
Db 923 SVLRGEGPNKGLPFIDDDYVATDDKVTDY 950
:||||| ||||| : :

RESULT 6
AB0088
probable flagellar M-ring protein flilF [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C;Accession: AB0088
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AB0088
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-546 <KUR>
A;Cross-references: UNIPROT:Q8Z108; UNIPARC:UPI000000DCD2A; GB:AL590842; PIDN:CA099565.1;
C;Genetics:
A;Gene: flfP
C;Superfamily: probable flagellar basal-body M ring protein

Query Match 36.2%; Score 50; DB 2; Length 546;
Best Local Similarity 72.7%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 LNKSLLPILHEW 18
|||||:|:|
DB 360 LNKSLLPVLQW 370

RESULT 7
T41645
probable spindle pole body-associating protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41645
R;Wood, V.; Rajandream, M.A.; Bartell, B.G.; Lucas, M.; Gaillardin, C.
submitted to the EMBL Data Library, January 1999
A;Reference number: 222006
A;Accession: T41645
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-809 <WOO>
A;Cross-references: UNIPROT:O94534; UNIPARC:UPI0000125794; EMBL:AL035247; PIDN:CAA22843.
A;Experimental source: strain 972h-; cosmid c895
C;Genetics:
A;Gene: SPDB:SPCC895.07
A;Map position: 3

Query Match 36.2%; Score 50; DB 2; Length 809;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 4 RGSINKSLPILHEWKFFDYDF 25
|:|:|:|:|:|:|
DB 303 RKEALDKLLPVLSPKIKDNDF 324

RESULT 8
G83914
hypothetical protein BH2119 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83914
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
submitted to the EMBL Data Library, January 1999
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83914
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-161 <STO>
A;Cross-references: UNIPROT:Q9KB16; UNIPARC:UPI000000C3DB1; GB:AP001514; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2119

Query Match 35.9%; Score 49.5; DB 2; Length 161;
Best Local Similarity 40.9%; Pred. No. 4.4;
Matches 9; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY 4 RGSINKSLPILHEWKFFDYDF 25
|:|:|:|:|:|:|
DB 99 KGEDIQTYQDLHW-LFDSY 119

RESULT 9
S57598

PEP5 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: ENL1 protein; protein YM9959.13; protein YMR231w
C;Species: Saccharomyces cerevisiae
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57598; S11188; S14460
R;Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57587
A;Accession: S57598
A;Molecule type: DNA
A;Residues: 1-1029 <SKE>
A;Cross-references: UNIPROT:PI2868; UNIPARC:UPI0000052FFA; EMBL:Z49939; NID:G887599; PID
A;Experimental source: strain AB972
R;Woolford, C.A.; Dixon, C.K.; Manolson, M.F.; Wright, R.; Jones, E.W.
Genetics 125, 739-752, 1990
A;Title: Isolation and characterization of PEP5, a gene essential for vacuolar biogenesis
A;Reference number: S11188; MUID:90375022; PMID:2204580
A;Accession: S11188
A;Molecule type: DNA
A;Residues: 1-138, 'K', 140-1023, 'E', 1024-1029 <WOO>
A;Cross-references: UNIPARC:UPI0000179046; EMBL:X54466
A;Experimental source: strain X2180-1B
A;Note: the authors translated the codon GAA for residue 121 as Ile, GAC for residue 139
R;Dulic, V.; Riezman, H.
EMBO J. 8, 1349-1359, 1989
A;Title: Characterization of the ENL1 gene required for vacuole biogenesis and gluconeog
A;Reference number: S14460; MUID:89356602; PMID:2670552
A;Accession: S14460
A;Molecule type: DNA
A;Residues: 1-36, 'R', 38-618, 'M', 620, 'FTVT', 624, 'H', 626-768, 'KQ', 771-1029 <DUL>
A;Cross-references: UNIPARC:UPI0000168BFE; EMBL:X15355; NID:G3679; PIDN:CAA33413.1; PID:
C;Genetics:
A;Gene: SGD:PEP5; ENL1
A;Cross-references: SGD:S0004844; MIPS:YMR231w
A;Map position: 13R
C;Function:
A;Description: required for gluconeogenic growth; involved in both the internalization a
C;Superfamily: Saccharomyces cerevisiae PEP5 protein
C;Keywords: transmembrane protein; yeast vacuole
F;139-155/Domain: transmembrane #status predicted <TM1>
F;310-326/Domain: transmembrane #status predicted <TM2>
F;454-470/Domain: transmembrane #status predicted <TM3>
F;661-677/Domain: transmembrane #status predicted <TM4>

Query Match 35.9%; Score 49.5; DB 2; Length 1029;
Best Local Similarity 40.0%; Pred. No. 38;
Matches 10; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

QY 1 NILRGESINKSLPILHEWKFFDYDF 25
|:|:|:|:|:|:|
DB 52 NIIKVKLNQS-QVIEFQSPPHDF 75
|:|:|:|:|:|:|

RESULT 10
T15925
hypothetical protein EEED8.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15925
R;Chissoe, S.
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid EEED8.
A;Reference number: Z18428
A;Accession: T15925
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-160 <CHI>
A;Cross-references: UNIPROT:Q19068; UNIPARC:UPI0000077B4F; EMBL:U23484; NID:G733597; PFI
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:EEED8.13
A;Introns: 20/3

Query Match 35.5%; Score 49; DB 2; Length 160;
Best Local Similarity 40.0%; Pred. No. 5.2;
Matches 8; Conservative 5; Mismatches 7; Indels

Qy 5 GESLNKSLPILHEWKFFDYD 24
| : | | | : : | : | : |
Db 18 GORLNSQLNLHSRKWIDFD 37

RESULT 11
B83743
N-ethylmaleline chlorohydrolase BH0746 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2004
C:Accession: B83743
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83743
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-445 <STO>
A;Cross-references: UNIPROT:Q9KEV3; UNIPARC:UPI000000C3991; GB:BA000004; NID
A;Experimental source: strain C-125
C:Genetics:
A;Gene: BH0746
C:Superfamily: metal-dependent hydrolase (amidohydrolase)

```
Query Match      35.5%; Score 49; DB 2; Length 445;
Best Local Similarity 47.1%; Pred. No. 17;
Matches 8: Conservative 4; Mismatches 5; Indels 0; Gaps 0;
```

Qy 6 ESLNKSPLIHEWKFFD 22
: : : : :
Db 165 OSIEXSIELLEEWHSFD 181

RESULT 12
AH1085
hypothetical protein lmo0087 [imported] - *Listeria monocytogenes* (strain EGD-e)
C:Species: *Listeria monocytogenes*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH1085
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1085
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-768 <GLA>
A:Cross-references: UNIPROT:Q8YAN0; UNIPARC:UPI00000554B7; GB:NC_003210; PIDN:CAC98302.1
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0087

Query Match 35.5%; Score 49; DB 2; Length 768;
Best Local Similarity 34.8%; Pred. No. 32;
Matches 8: Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 NILRGESLNKSLPILHEWKFFDY 23
|- :|:| | : :| :|
Db 540 NLKASQSVNKVLQVQYDWSSADY 562

RESULT 13
S51796
vasodilator-stimulated phosphoprotein VASP - dog

C/Species: Canis lupus familiaris (dog)
C/Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S51796
R/Haffner, C.; Jarchau, T.; Reinhard, M.; Hoppe, J.; Lohmann, S.M.; Walter,
EMBO J. 14, 19-27, 1995
A/Title: Molecular cloning, structural analysis and functional expression o
A/Reference number: S51796; MUID:95129547; PMID:7828592
A/Accession: S51796
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-384 <HAF>
A/Cross-references: UNIPROT:P50551; UNIPARC:UPI0000138121; EMBL:Z46388; NID
C/Keywords: phosphoprotein

Query Match	34.8%	Score 48;	DB 2;	Length 384;
Best Local Similarity	38.9%	Pred. No. 21;		
Matches	7;	Mismatches	5;	Gaps
Conservative		Indels	6;	

Qy 2 ILRGESLNKSLPIHLEWK 19
|:|:| |::| |::|:
Db 66 IVRGIKYNQATPTTFHOWR 83

RESULT 14
S54020
probable membrane protein YMR019w - yeast (Saccharomycetes cerevisiae)
N:Alternate names: hypothetical protein YM9711.08
C:Species: Saccharomycetes cerevisiae
C/Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Oct-2004
C/Accession: S54020
R:Lye, G.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54014
A:Accession: S54020
A:Molecule type: DNA
A:Residues: 1-949 <LYE>
A:Cross-references: UNIPROT:P50104; UNIPARC:UPI00001360AE; EMBL:Z49211; NID
A:Experimental source: strain A9972

Query Match	34.8%	Score 48;	DB 2;	Length 949;
Best Local Similarity	42.9%	Pred. No. 59;		
Matches	9;	Mismatches	5;	Gaps
Conservative	9;	Indels	7;	

Qy 4 RGESLNKSLPILHENWKFFDYD 24
::: ||| |||::|
pb 369 KGDERSOEKNIRHESKFFEDF 389

RESULT 15
S51797
vasodilator-stimulated phosphoprotein - human
C:Species: Homo sapiens (man)
C:Date: 15-Jul-1995 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C:Accession: S51797; S55526
F:Haefliger, C.; Jarchau, T.; Reinhard, M.; Hoppe, J.; Lohmann, S.M.; Walter,
EMBO J. 14, 19-27, 1995
A:Title: Molecular cloning, structural analysis and functional expression c
A:Reference number: S51796; MUID:95129547; PMID:7828592

A;Residues: 1-380 <HAF1>
A;Cross-references: UNIPROT:P50552; UNIPARC:UPI0000001C69; EMBL:Z46389; NID:5624963; PDB:1W83
A;Accession: S55326
A;Molecule type: protein
A;Residues: 11-35;87-96;140-154;255-282;297-303;305-322 <HAF2>

A;Cross-references: UNIPARC:UPI000017C415; UNIPARC:UPI000017C416; UNIPARC:UPI000017C417;
C;keywords: phosphoprotein

Query Match 34.1%; Score 47; DB 2; Length 380;
Best Local Similarity 38.9%; Pred. No. 29;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 ILRGESLNKSLPILHEWK 19
|:| |::| |:|
Db 66 IVRGVKYNQATPNFQWR 83

Search completed: May 3, 2006, 19:10:18
Job time : 2.87757 secs

This page blank (uspo)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 18:54:38 ; Search time 11.5741 Seconds
(without alignments)
1523.941 Million cell updates/sec

Title: US-10-525-567-2

Perfect score: 138

Sequence: 1 NLRGESLNKSLPIHEWKFFDYDF 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	432	1	MRJPI_APIME
2	138	100.0	432	2	Q548D6_APIME
3	124	89.9	222	2	Q51224_APICE
4	124	89.9	433	2	Q5VLE2_APICE
5	124	89.9	433	2	Q8MMJ1_APICE
6	84	60.9	452	1	MRJPI2_APIME
7	76.5	55.4	443	2	Q8IMJ9_APICE
8	75.5	54.7	220	2	Q51223_APICE
9	74	53.6	463	2	Q8MMJ0_APICE
10	74	53.6	463	2	Q5OH66_APICE
11	74	53.6	468	2	Q5VK55_APICE
12	73	52.9	464	1	MRJPA_APIME
13	71	51.4	437	2	Q8W3E3_APIME
14	70	50.7	416	2	Q5TGR0_APIME
15	69	50.0	222	2	Q51222_APICE
16	69	50.0	485	2	Q6QNT6_APICE
17	69	50.0	579	2	Q6QNT5_APICE
18	69	50.0	598	2	Q5VK56_APICE
19	68	49.3	598	1	MRJPS_APIME
20	60	43.5	274	2	Q8TKD5_METAC
21	57	41.3	131	2	Q9D261_MOUSE
22	55.5	40.2	768	2	Q35266_RAT
23	55	39.9	375	1	VASP_MOUSE
24	55	39.9	375	2	Q91VD2_MOUSE
25	55	39.9	544	1	MRJPI_APIME
26	54.5	39.5	509	1	MATK_SCHTR
27	53	38.4	310	2	Q8IA99_CAEL
28	53	38.4	425	2	Q76258_CAEL
29	53	38.4	454	2	Q8IAA0_CAEL
30	53	38.4	468	2	Q8IT88_CAEL
31	52	37.7	536	2	Q6C7B7_YARLLI

32	52	37.7	712	2	Q6BU38_DEBHA
33	52	37.7	1072	2	Q4WXA3_ASPPU
34	51	37.0	281	2	Q6G7T5_STAAS
35	51	37.0	281	2	Q5HEH8_STAAC
36	51	37.0	281	2	Q8NVL6_STAAM
37	51	37.0	495	2	Q8D7I4_VIBVU
38	51	37.0	1250	2	Q5B8W8_EMENI
39	50.5	36.6	869	1	YD95_YEAST
40	50.5	36.6	1115	1	YAA4_SCHPO
41	50	36.2	240	2	Q82S24_NITEU
42	50	36.2	423	2	Q4ZJX1_APIME
43	50	36.2	546	2	Q8Z108_YERPE
44	50	36.2	546	2	Q666B0_YERPS
45	50	36.2	809	1	ALP14_SCHPO

Q6bu38 debaryomyce
Q4wxa3 aspergillus
Q6g7t5 staphylococ
Q5heh8 staphylococ
Q8nvl6 staphylococ
Q8d7i4 vibrio vuln
Q5b8w8 aspergillus
YD95 saccharomyc
Q82s24 schizosacch
Q4zjx1 apis mellif
Q8z108 yersinia pe
Q666b0 yersinia ps
Q94534 schizosacch

ALIGNMENTS

RESULT 1

MRJPI_APIME
ID MRJPI_APIME STANDARD; PRT; 432 AA.

AC O18330;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Major royal jelly protein 1 precursor (MRJP-1) (Bee-milk protein).

GN Names=MRJPI;

OS Apis mellifera (Honeybee).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apoidea; Apoidea;

OC Apidae; Apis.

OX NCBI_TaxID=7460;

RN [1]

RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 39-48; 63-71 AND 361-380.

RC TISSUE=Hypopharyngeal gland;

RX MEDLINE=98055707; PubMed=9395329;

RA Ohashi K., Natori S., Kubo T.;

RT "Change in the mode of gene expression of the hypopharyngeal gland

cells with an age-dependent role change of the worker honeybee Apis

mellifera L.";

RL Eur. J. Biochem. 249:797-802(1997).

RN [2]

RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 20-30.

RC TISSUE=Head;

RX MEDLINE=99007754; PubMed=9791542; DOI=10.1007/s000180050229;

RA Schmitzova J., Klaudivny J., Albert S., Schroeder W., Schreckengost W.,

Hanes J., Judova J., Simuth J.;

RT "A family of major royal jelly proteins of the honeybee Apis mellifera

L.";

RL Cell. Mol. Life Sci. 54:1020-1030(1998).

CC -!- FUNCTION: May play an important role in honeybee nutrition. Most

abundant protein found in the royal jelly which is the food of the

queen honey bee larva. The royal jelly determines the development

of the young larvae and is responsible for the high reproductive

ability of the honeybee queen.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Found in the hypopharyngeal glands of the

worker honeybee.

CC -!- DEVELOPMENTAL STAGE: Produced in the cephalic glands of both the

nurse bee and the forager bee. This bee milk protein changes to

alpha-glucosidase in accordance with the age-dependent role change

of the worker bee.

CC -!- SIMILARITY: Belongs to the major royal jelly protein family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use as long as its content is in no way modified and this statement is not

removed.

CC EMBL; D79207; BAA23639.1; -; mRNA.

CC EMBL; AF000633; AAC61895.1; -; mRNA.

DR

```

DR Ensembl; ENSAPMG0000007331; Apis mellifera.
DR InterPro; IPR009007; Pept Aspartic_cat.
DR InterPro; IPR003534; Royaljelly.
DR PANTHER; PTHR10009; Royaljelly; 1.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW Direct protein sequencing; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 432 Major royal jelly protein 1.
FT CARBOHYD 28 28 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 144 144 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 177 177 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 432 AA; 48886 MW; 9F42BF08D34A1A7B CRC64;

Query Match 100.0%; Score 138; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIIRGESLNKSLPILHEWKFFDYDF 25
   |||||
Db 20 NIIRGESLNKSLPILHEWKFFDYDF 44

RESULT 2
Q548D6_APIME
ID Q548D6_APIME PRELIMINARY; PRT; 432 AA.
AC Q548D6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Major royal jelly protein MRJP1.
OS Apis mellifera (Honeybee).
GN Name=mrjp1;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
OX NCBI_TaxID=7460;
RN [1]

NUCLEOTIDE SEQUENCE.
RP MDLINE=22448659; PubMed=12559578; DOI=10.1016/S0378-1119(02)01174-5;
RX Malecova B., Ramser J., O'Brien J.K., Janitz M., Judova J.,
RA Lehrach H., Simuth J.;
RT "Honeybee (Apis mellifera L.) mrjp gene family: computational analysis
of putative promoters and genomic structure of mrjp1, the gene coding
for the most abundant protein of larval food.";
RL Gene 303:165-175(2003).
DR EMBL; AF388203; AAM73637.1; -; Genomic DNA.
SQ SEQUENCE 432 AA; 48886 MW; 9F42BF08D34A1A7B CRC64;

Query Match 100.0%; Score 138; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIIRGESLNKSLPILHEWKFFDYDF 25
   |||||
Db 20 NIIRGESLNKSLPILHEWKFFDYDF 44

RESULT 3
Q51224_APICE
ID Q51224_APICE PRELIMINARY; PRT; 222 AA.
AC Q51224;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Major royal jelly protein 1 (Fragment).
GN Name=MRJP1;
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
OX NCBI_TaxID=7461;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RA Su S., Albert S., Chen S., Zhong B.;
RT "Molecular cloning and analysis of four cDNAs from the heads of Apis
cerana cerana nurse honeybees coding for major royal jelly proteins.";
RL Apidologie 36:389-401(2005).
DR EMBL; AY862495; AAW51950.1; -; Genomic DNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
FT NON_TER 1 1
FT NON_TER 222 222
SQ SEQUENCE 222 AA; 24696 MW; 364E43FC74DA3EA2 CRC64;

Query Match 89.9%; Score 124; DB 2; Length 222;
Best Local Similarity 88.0%; Pred. No. 2e-10;
Matches 22; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIIRGESLNKSLPILHEWKFFDYDF 25
   :|||||
Db 12 SILRGESLNKSLSVLHEWKFFDYDF 36

RESULT 4
Q5VLE2_APICC
ID Q5VLE2_APICC PRELIMINARY; PRT; 433 AA.
AC Q5VLE2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Major royal jelly protein MRJP1.
OS Apis cerana cerana (Oriental honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
OX NCBI_TaxID=94128;
RN [1]

NUCLEOTIDE SEQUENCE.
RP TISSUE=Head;
RX Songkun S., Shenglu C., Stefan A., Boxiong Z.;
RT "Molecular Cloning of MRJP1 cDNA from Apis cerana cerana in China.";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV279539; AAQ16677.1; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
SQ SEQUENCE 433 AA; 49045 MW; 86D6C115EF40B9B5 CRC64;

Query Match 89.9%; Score 124; DB 2; Length 433;
Best Local Similarity 88.0%; Pred. No. 4.3e-10;
Matches 22; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIIRGESLNKSLPILHEWKFFDYDF 25
   :|||||
Db 21 SILRGESLNKSLSVLHEWKFFDYDF 45

RESULT 5
Q8MMJ1_APICE
ID Q8MMJ1_APICE PRELIMINARY; PRT; 433 AA.
AC Q8MMJ1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Major royal jelly protein MRJP1 precursor (Major royal jelly protein
1).
GN Name=MRJP1; Synonyms=mrjp1;
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
OX NCBI_TaxID=7461;
RN [1]

NUCLEOTIDE SEQUENCE.

```

```

DR PFam: PF03022; MRJP; 1.
DR PRINTS: PR01366; ROYALJELLY.
DR Direct protein sequencing; Glycoprotein; Signal.
KW SIGNAL
FT 1 17
FT CHAIN 18 452 Major royal jelly protein 2.
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
FT SEQUENCE 452 AA; 51074 MW; 25E5B621288FE189 CRC64;
SQ
Query Match 60.9%; Score 84; DB 1; Length 452;
Best Local Similarity 68.4%; Pred. No. 0.00057;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 SLNKSPLILHEWKFFDYDF 25
   :| || ||| :||| :||| |||
Db 27 NLEKSLNVHIEWKYFDYDF 45

RESULT 7
Q6IMJ9 APIME PRELIMINARY; PRT; 443 AA.
ID Q6IMJ9;
AC Q6IMJ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Major royal jelly protein 7.
GN Names=MRJP7;
OS Apis mellifera (Honeybee).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OC NCBI_TaxID=7460;
OX
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15037093; DOI=10.1016/j.jinsphys.2003.09.008;
RA Albert S., Klaudiny J.;
RT "The MRJP/YELLOW protein family of Apis mellifera: identification of
RT new members in the EST library.";
RL J. Insect Physiol. 50:51-59(2004).
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK001420; DAA01512.1; -; mRNA.
DR Ensembl; ENSAPMG0000007331; Apis mellifera.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
DR SEQUENCE 443 AA; 50541 MW; 8916272B4ADB421 CRC64;

Query Match 55.4%; Score 76.5; DB 2; Length 443;
Best Local Similarity 55.6%; Pred. No. 0.0078;
Matches 19; Conservative 3; Mismatches 6; Indels 3; Gaps 1

QY 2 ILRGES---LNKSLPILHEWKFFDYDF 25
   ||| | | | | | | | | | | | | | |
Db 19 ILRENSARNLKNSLVKMHENKYIDYDF 45

RESULT 8
Q51223 APICE PRELIMINARY; PRT; 220 AA.
ID Q51223;
AC Q51223;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Major royal jelly protein 7 (Fragment).
GN Name=MRJP7;
OS Apis cerana (Indian honeybee).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OC NCBI_TaxID=7461;
OX
RN NUCLEOTIDE SEQUENCE.
RP

```

```
RA Su S., Albert S., Chen S., Zhong B.;
RT "Molecular cloning and analysis of four cDNAs from the heads of Apis
RT cerana cerana nurse honeybees coding for major royal jelly proteins.";
RL Apidologie 36:389-401(2005).
DR EMBL; AY862496; AAW51951.1; -; Genomic_DNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PRO1366; ROYALJELLY.
FT NON TER 220 220
FT NON TER 1
SQ SEQUENCE 220 AA; 24927 MW; 7EC00E3E7AAA6822 CRC64;

Query Match 54.7%; Score 75.5; DB 2; Length 220;
Best Local Similarity 55.6%; Pred. No. 0.0051;
Matches 15; Conservative 4; Mismatches 5; Indels 3; Gaps 1;

QY 2 ILRGES---LNKSLPILHEWKFFDYDF 25
Db 10 IVRKSNRLNSLNVLHWEWKYIDYDF 36

RESULT 9
Q8MJA0.APICE PRELIMINARY; PRT; 463 AA.
AC Q8MJA0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Major royal jelly protein MRJP2 precursor.
DE Name=MRJP2;
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
OX NCBI_TaxID=7461;
RN [1];
RP TISSUE=Nurse heads;
RC Sittipraneed S., Injongjirak C.;
RA "Molecular Cloning of Major Royal Jelly Protein (MRJP2) cDNA from Apis
RT cerana in Thailand.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF525777; AAM88282.2; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PRO1366; ROYALJELLY.
KW Signal.
FT SIGNAL 1 17 Potential.
FT SIGNAL 1 17 Potential.
SQ SEQUENCE 463 AA; 52490 MW; 29D92E3749B15992 CRC64;

Query Match 53.6%; Score 74; DB 2; Length 463;
Best Local Similarity 55.0%; Pred. No. 0.02;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 6 ESLNKSILPILHEWKFFDYDF 25
Db 26 KNLNSLNVLHWEWKYIDYDF 45

RESULT 10
Q50H66.APICE PRELIMINARY; PRT; 463 AA.
AC Q50H66;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Major royal jelly protein 2.
DE Name=mrjpl;
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
OX NCBI_TaxID=7461;
```

```
RN NUCLEOTIDE SEQUENCE.
RP Injongjirak C., Klinbunga S., Sittipraneed S.;
RT "Cloning, Expression and Genomic Organization of Genes Encoding Major
RT Royal Jelly Protein 1 and 2 of the Honeybee (Apis cerana).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY515689; AAS88557.1; -; Genomic_DNA.
SQ SEQUENCE 463 AA; 52462 MW; 930C91C8CC595935 CRC64;

Query Match 53.6%; Score 74; DB 2; Length 463;
Best Local Similarity 55.0%; Pred. No. 0.02;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 6 ESLNKSILPILHEWKFFDYDF 25
Db 26 KNLNSLNVLHWEWKYIDYDF 45

RESULT 11
Q5VK55.APICC PRELIMINARY; PRT; 468 AA.
AC Q5VK55;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Major royal jelly protein MRJP2.
DE OS Apis cerana cerana (Oriental honeybee).
DE OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
DE OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
DE OC Apoidea; Apis.
DE OX NCBI_TaxID=94128;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RA Su S., Chen S., Albert S.;
RT "Molecular cloning of MRJP2 cDNA from Apis cerana cerana in China.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY392758; AAR83083.1; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PRO1366; ROYALJELLY.
SQ SEQUENCE 468 AA; 53060 MW; 5B2A6AEP4C530C84 CRC64;

Query Match 53.6%; Score 74; DB 2; Length 468;
Best Local Similarity 55.0%; Pred. No. 0.02;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 6 ESLNKSILPILHEWKFFDYDF 25
Db 26 KNLNSLNVLHWEWKYIDYDF 45

RESULT 12
MRJP4.APIME STANDARD; PRT; 464 AA.
AC Q17061;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Major royal jelly protein 4 precursor (MRJP-4) (Bee-milk protein)
DE (Royal jelly protein RJP57-2).
DE Name=MRJP4;
GN Apis mellifera (Honeybee).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
OX NCBI_TaxID=7460;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Head;
RA Klaudiny J., Hanes J., Kulifajova J., Albert S., Simuth J.;
RT "Molecular cloning of two cDNAs from the head of the nurse honey bee
RT (Apis mellifera L.) for coding related proteins of royal jelly.";
RT J. Apicultural Res. 33:105-111 (1994).
```



```
RL Apidologie 36:389-401(2005).
DR ENBL; AY862497; AAW51952.1; -; Genomic_DNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
FT NON_TER 222 222
SQ SEQUENCE 222 AA; 24877 MW; B37705F4570C549F CRC64;

Query Match      50.0%; Score 69; DB 2; Length 222;
Best Local Similarity 52.6%; Pred.No; 0.05;
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      7 SLNKSFLPILHEWKFFDYDF 25
      :| | : :| | | :| | |
Db      21 NLANSNMVNIHEWKYLDYDF 39

Search completed: May 3, 2006, 19:09:00
Job time : 13.5741 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:09:24 ; Search time 2.70062 Seconds
(without alignments)
765.341 Million cell updates/sec

Title: US-10-525-567-2

Perfect score: 138

Sequence: 1 NILRGESLNKSLPILHEWKFFDYDF 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5 COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	36.2	696	2	US-09-248-796A-16205
2	49.5	35.9	274	2	US-08-256-847C-4
3	49.5	35.9	411	2	US-09-328-352-5039
4	49.5	35.9	610	2	US-09-328-352-7804
5	48	34.8	469	2	US-09-248-796A-16207
6	48	34.8	508	2	US-09-248-796A-16204
7	47.5	34.4	204	2	US-09-914-098-40
8	47	34.1	116	2	US-09-377-285B-69
9	47	34.1	116	2	US-10-192-381-69
10	47	34.1	378	1	US-08-986-217-6
11	47	34.1	380	1	US-09-026-587-4
12	47	34.1	380	1	US-09-227-420-4
13	47	34.1	380	1	US-09-387-811-4
14	47	34.1	380	2	US-09-823-240A-10
15	47	34.1	381	2	US-09-949-016-7291
16	47	34.1	635	2	US-09-417-197-125
17	46.5	33.7	444	2	US-10-104-047-2354
18	46	33.3	115	2	US-09-377-285B-67
19	46	33.3	115	2	US-10-192-381-67
20	46	33.3	232	2	US-09-328-352-5918
21	46	33.3	314	2	US-09-540-236-2699
22	46	33.3	393	1	US-09-026-587-3
23	46	33.3	393	1	US-09-227-420-3
24	46	33.3	393	2	US-09-387-811-3
25	46	33.3	393	2	US-09-823-240A-11
26	46	33.3	418	1	US-09-026-587-1
27	46	33.3	418	1	US-09-227-420-1

28	46	33.3	418	2	US-09-387-811-1	Sequence 1, Appli
29	46	33.3	705	2	US-09-198-452A-68	Sequence 68, Appl
30	46	33.3	705	2	US-09-438-185A-50	Sequence 50, Appl
31	45	32.6	166	2	US-09-732-210-702	Sequence 702, App
32	44.5	32.2	1786	1	US-08-477-451-16	Sequence 16, Appl
33	44	31.9	240	2	US-09-355-166-19	Sequence 19, Appl
34	44	31.9	305	2	US-10-012-231A-273	Sequence 273, App
35	44	31.9	305	2	US-10-015-389A-273	Sequence 273, App
36	44	31.9	305	2	US-10-006-768A-273	Sequence 273, App
37	44	31.9	305	2	US-10-015-671A-273	Sequence 273, App
38	44	31.9	305	2	US-10-015-393A-273	Sequence 273, App
39	44	31.9	305	2	US-10-011-833A-273	Sequence 273, App
40	44	31.9	305	2	US-10-006-041A-273	Sequence 273, App
41	44	31.9	305	2	US-10-012-064A-273	Sequence 273, App
42	44	31.9	333	2	US-09-107-532A-4698	Sequence 4698, Ap
43	44	31.9	389	2	US-09-270-767-46824	Sequence 46824, A
44	44	31.9	481	2	US-09-215-694-17	Sequence 17, Appl
45	44	31.9	481	2	US-10-109-310-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-248-796A-16205
; Sequence 16205, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16205
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16205

Query Match 36.2%; Score 50; DB 2; Length 696;
Best Local Similarity 38.7%; Pred. No. 11;
Matches 12; Conservative 6; Mismatches 7; Indels 6; Gaps 1;

Qy 1 NILRGESLNKSL-----PILHEWKFFDYDF 25
Db 189 SILPGLANKYLTMLARKEIINGWKISSYNF 219

RESULT 2
US-08-256-847C-4
; Sequence 4, Application US/08256847C
; Patent No. 6403099
; GENERAL INFORMATION:
; APPLICANT: Rappuoli, Rino
; APPLICANT: Costantino, Paolo
; APPLICANT: No. 6403099elli, Francesco
; TITLE OF INVENTION: Conjugates Formed From Heat Shock Proteins And Oligo or Polysacch
; FILE REFERENCE: CHIR-0042
; CURRENT APPLICATION NUMBER: US/08/256,847C
; CURRENT FILING DATE: 1994-11-01
; PRIOR APPLICATION NUMBER: PCT/EP93/00516
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: F192A000058
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

```
; LENGTH: 274
; TYPE: PRT
; ORGANISM: M. leprae
US-08-256-847C-4

Query Match      35.9%; Score 49.5; DB 2; Length 274;
Best Local Similarity 45.5%; Pred. No. 4.5;
Matches 10; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

Qy 4 RGSLSKSLPILHEW-KFFDYD 24
   ||||| : : : : :
Db 54 RGERLSALKVLEKWNIWYDYE 75

RESULT 3
US-09-328-352-5039
; Sequence 5039, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5039
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5039

Query Match      35.9%; Score 49.5; DB 2; Length 411;
Best Local Similarity 52.2%; Pred. No. 7.2;
Matches 12; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NIIRGESLKSILPILHEWKFFDY 23
   | : | | | | | : | : | : |
Db 252 NVLNRSLNTHLEALHEQQ-FDY 273

RESULT 4
US-09-328-352-7804
; Sequence 7804, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7804
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7804

Query Match      35.9%; Score 49.5; DB 2; Length 610;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 10; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 10 KSLPILH-EWKFFDYD 24
   | | | | | | | | | |
Db 588 KGHPLHAEMWYFDID 603

RESULT 5
US-09-248-796A-16207
; Sequence 16207, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
```

```
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; ORGANISM: Candida albicans
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16207
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16207

Query Match      34.8%; Score 48; DB 2; Length 469;
Best Local Similarity 35.5%; Pred. No. 15;
Matches 11; Conservative 7; Mismatches 7; Indels 6; Gaps 1;

Qy 1 NIIRGESLKS-----PILHEWKFFDYDF 25
   : || | : || | : : : | : | : |
Db 331 SILPGLALNKLTLPKKEVINGWKISGYNF 361

RESULT 6
US-09-248-796A-16204
; Sequence 16204, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16204
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (487),(503),(504),(506)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-16204

Query Match      34.8%; Score 48; DB 2; Length 508;
Best Local Similarity 35.5%; Pred. No. 17;
Matches 11; Conservative 7; Mismatches 7; Indels 6; Gaps 1;

Qy 1 NIIRGESLKS-----PILHEWKFFDYDF 25
   : || | : || | : : : | : | : |
Db 301 SILPGLALNKLTLPKKEVINGWKISGYNF 331

RESULT 7
US-09-914-098-40
; Sequence 40, Application US/09914098
; Patent No. 6855863
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Lysophosphatidic Acid Acetyltransferases
; FILE REFERENCE: BH1332
; CURRENT APPLICATION NUMBER: US/09/914,098
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/121,119
; PRIOR FILING DATE: 1999-02-22
```



```

; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 40
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (68)
; OTHER INFORMATION: Xaa = any amino acid
US-09-914-098-40

Query Match          34.1%; Score 47.5; DB 2; Length 204;
Best Local Similarity 47.1%; Pred. No. 6.8;
Matches 8; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 7 SLNKSPLPILHEWKFFDY 23
Db 168 ALN-ALPTYYSWRFPDY 183

RESULT 8
US-09-377-285B-69
; Sequence 69, Application US/09377285B
; Patent No. 6720175
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENEKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)
; FILE REFERENCE: JHU1580-4
; CURRENT APPLICATION NUMBER: US/09/377,285B
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-377-285B-69

Query Match          34.1%; Score 47; DB 2; Length 116;
Best Local Similarity 38.9%; Pred. No. 4.2;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 ILRGESLNKSLPILHEWK 19
Db 66 IVRGVKYNQATPFPQWR 83

RESULT 9
US-10-192-381-69
; Sequence 69, Application US/10192381
; Patent No. 6864083
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENEKEN, Jutta
```

```

; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)
; FILE REFERENCE: JHU1580-4
; CURRENT APPLICATION NUMBER: US/10/192,381
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-192-381-69

Query Match          34.1%; Score 47; DB 2; Length 116;
Best Local Similarity 38.9%; Pred. No. 4.2;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 ILRGESLNKSLPILHEWK 19
Db 66 IVRGVKYNQATPFPQWR 83

RESULT 10
US-08-986-217-6
; Sequence 6, Application US/08986217
; Patent No. 5914249
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: CELL-CYCLE PHOSPHOPROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,217
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0452 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1617319
US-08-986-217-6

Query Match          34.1%; Score 47; DB 1; Length 378;
Best Local Similarity 38.9%; Pred. No. 17;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ILRGESLNKSLPILHEWK 19
Db 64 IVRGVKYNQATPNFQWR 81

RESULT 11
US-09-026-587-4
; Sequence 4, Application US/09026587
; Patent No. 5912128
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN ENA/VASP-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,420
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/026,587
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0471 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 624964
US-09-227-420-4

Query Match          34.1%; Score 47; DB 1; Length 380;
Best Local Similarity 38.9%; Pred. No. 17;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ILRGESLNKSLPILHEWK 19
Db 66 IVRGVKYNQATPNFQWR 83

RESULT 13
US-09-387-811-4
; Sequence 4, Application US/09387811
; Patent No. 6645499
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN ENA/VASP-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
```

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,811
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,587
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0471 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 624964
US-09-387-811-4
Query Match 34.1%; Score 47; DB 2; Length 380;
Best Local Similarity 38.9%; Pred. No. 17;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Qy 2 ILRGESLNKSLPILHEWK 19
|:|:| |:| |:| |:|
Db 66 IVRGVKNQATPNFHQWR 83
Search completed: May 3, 2006, 19:12:05
Job time : 3.70062 secs

RESULT 15
US-09-949-016-7291
; Sequence 7291, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7291
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7291
Query Match 34.1%; Score 47; DB 2; Length 381;
Best Local Similarity 38.9%; Pred. No. 17;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Qy 2 ILRGESLNKSLPILHEWK 19
|:|:| |:| |:| |:|
Db 67 IVRGVKNQATPNFHQWR 84
Search completed: May 3, 2006, 19:12:05
Job time : 3.70062 secs

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,811
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,587
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0471 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 624964
US-09-387-811-4
Query Match 34.1%; Score 47; DB 2; Length 380;
Best Local Similarity 38.9%; Pred. No. 17;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Qy 2 ILRGESLNKSLPILHEWK 19
|:|:| |:| |:| |:|
Db 66 IVRGVKNQATPNFHQWR 83
Search completed: May 3, 2006, 19:12:05
Job time : 3.70062 secs

RESULT 14
US-09-823-240A-10
; Sequence 10, Application US/09823240A
; Patent No. 6716597
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James B. Bear
; APPLICANT: Jurgen Wehland
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; Motility
; FILE REFERENCE: M00656.70064 US
; CURRENT APPLICATION NUMBER: US/09/823,240A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-823-240A-10
Query Match 34.1%; Score 47; DB 2; Length 380;
Best Local Similarity 38.9%; Pred. No. 17;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Qy 2 ILRGESLNKSLPILHEWK 19
|:|:~ |:| |:| |:|
Db 66 IVRGVKNQATPNFHQWR 83
Search completed: May 3, 2006, 19:12:05
Job time : 3.70062 secs

the Page Mark (uplo)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:10:39 ; Search time 8.77058 Seconds
(without alignments)
1190.997 Million cell updates/sec

Title: US-10-525-567-2
Perfect score: 138
Sequence: 1 NIURGESLNKSLPILHWEKFFDYDF 25

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	39.9	79	4	US-10-424-599-242162
2	52	37.7	42	3	US-09-764-877-1036
3	52	37.7	42	4	US-10-242-515-1036
4	52	37.7	168	4	US-10-424-599-180168
5	51	37.0	533	4	US-10-425-115-266449
6	49.5	35.9	255	4	US-10-282-122A-44667
7	49	35.5	142	4	US-10-418-861B-46
8	49	35.5	768	4	US-10-282-122A-60551
9	48	34.8	152	4	US-10-437-963-106441
10	48	34.8	439	4	US-10-424-599-190654
11	48	34.8	445	4	US-10-425-114-37354
12	48	34.8	541	4	US-10-437-963-106443
13	48	34.8	904	4	US-10-032-585-7917
14	48	34.8	949	4	US-10-149-310-206
15	47	34.1	46	4	US-10-425-115-201291
16	47	34.1	85	4	US-10-193-144-69
17	47	34.1	85	4	US-10-345-072-69
18	47	34.1	116	4	US-10-192-381-69
19	47	34.1	116	6	US-11-008-889-69
20	47	34.1	242	4	US-10-425-114-45051
21	47	34.1	242	4	US-10-425-114-53535
22	47	34.1	380	3	US-09-823-240-10
23	47	34.1	380	4	US-10-311-093-1
24	47	34.1	380	4	US-10-618-538-4
25	47	34.1	571	4	US-10-424-599-144073
26	47	34.1	635	4	US-10-072-036-125
27	47	34.1	1088	4	US-10-437-963-204592

28	47	34.1	1628	4	US-10-437-963-170587	Sequence 170587,
29	46.5	33.7	63	4	US-10-437-963-189474	Sequence 189474,
30	46.5	33.7	145	3	US-09-764-868-1233	Sequence 1233, Ap
31	46.5	33.7	444	4	US-10-104-047-2354	Sequence 2354, Ap
32	46.5	33.7	720	4	US-10-156-761-14403	Sequence 14403, A
33	46	33.3	115	6	US-10-192-381-67	Sequence 67, Appl
34	46	33.3	115	6	US-11-008-889-67	Sequence 280563,
35	46	33.3	140	4	US-10-424-599-280563	Sequence 45251, A
36	46	33.3	149	4	US-10-425-114-46739	Sequence 46739, A
37	46	33.3	225	4	US-10-282-122A-45251	Sequence 337842,
38	46	33.3	297	4	US-10-425-115-337842	Sequence 43907, A
39	46	33.3	301	4	US-10-767-701-43907	Sequence 11, Appl
40	46	33.3	310	4	US-10-223-074-11	Sequence 256290,
41	46	33.3	317	4	US-10-424-599-256290	Sequence 63074, A
42	46	33.3	333	4	US-10-282-122A-63074	Sequence 403, Appl
43	46	33.3	386	4	US-10-177-293-403	Sequence 11, Appl
44	46	33.3	393	3	US-09-823-240-11	Sequence 3,
45	46	33.3	393	4	US-10-618-538-3	Appli

ALIGNMENTS

RESULT 1
US-10-424-599-242162
; Sequence 242162, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 242162
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_606C.1.pep
US-10-424-599-242162

Query Match 39.9%; Score 55; DB 4; Length 79;
Best Local Similarity 46.2%; Pred. No. 2.2;
Matches 12; Conservative 2; Mismatches 4; Indels 8; Gaps 1;

Qy 4 RGESLNKSLP-----ILHWEKFF 21
|||:|||||:|||||
Db 25 RGSLNKKNPNPFLPVPVVLKEWAF 50

RESULT 2
US-09-764-877-1036
; Sequence 1036, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1036
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

```
; NAME/KEY: SITE
; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1036

Query Match          37.7%; Score 52; DB 3; Length 42;
Best Local Similarity 50.0%; Pred. No. 3.2;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 LRGESLNKSLPILHEWKF 20
   ||| : ||| : |||
Db 6 LRGRVINIHLFPVQKWKF 23

RESULT 3
US-10-242-515-1036
; Sequence 1036, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1036
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (33)_feature
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-515-1036

Query Match          37.7%; Score 52; DB 4; Length 42;
Best Local Similarity 50.0%; Pred. No. 3.2;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 LRGESLNKSLPILHEWKF 20
   ||| : ||| : |||
Db 6 LRGRVINIHLFPVQKWKF 23

RESULT 4
US-10-424-599-180168
; Sequence 180168, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
```

```
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 180168
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(168)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_133706C.1.pap
US-10-424-599-180168

Query Match          37.7%; Score 52; DB 4; Length 168;
Best Local Similarity 40.0%; Pred. No. 13;
Matches 10; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 NLRGESLNKSLPILHEWKFDDYDF 25
   :: ||| : ||| : |||
Db 144 SVSNGSLLDXKLEIPDEWKAHDFDF 168

RESULT 5
US-10-425-115-266449
; Sequence 266449, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 266449
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(533)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_174603C.1.pap
US-10-425-115-266449

Query Match          37.0%; Score 51; DB 4; Length 533;
Best Local Similarity 53.3%; Pred. No. 63;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 ESLNKSILPILHEWKF 20
   | : ||| : |||
Db 315 EPSKMNPLLLHEWRF 329

RESULT 6
US-10-282-122A-44667
; Sequence 44667, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
```

```

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44667
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-10-282-122A-44667

Query Match 35.9%; Score 49.5; DB 4; Length 255;
Best Local Similarity 52.2%; Pred. No. 49;
Matches 12; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

Qy 1 NILRGESLNKSLPILHEWKFFDY 23
Db 96 NVLNRSLNTHLEALHEQQ-FDY 117

RESULT 7
US-10-418-861B-46
; Sequence 46, Application US/10418861B
; Publication No. US20040010131A1
; GENERAL INFORMATION:
; APPLICANT: da Silva, Ana Claudia Rasera
; APPLICANT: Farah, Shaker Chuck
; APPLICANT: Quaggio, Ronaldo Bento
; APPLICANT: Reinach, Fernando de Castro
; APPLICANT: Ferro, Jesus Aparecido
; APPLICANT: De Oliveira, Julio Cezar Franco
; APPLICANT: De Laia, Marcelo Luiz
; APPLICANT: Setubal Joao C.
; APPLICANT: Furlan, Luiz Roberto
; TITLE OF INVENTION: Isolated Xanthomonas nucleic acid molecules, proteins encoded the
; FILE REFERENCE: uses thereof
; CURRENT APPLICATION NUMBER: US/10/418,861B
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/374,620
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 85

```

```

; SEQ ID NO 46
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Xanthomonas
; FEATURE:
US-10-418-861B-46

Query Match 35.5%; Score 49; DB 4; Length 142;
Best Local Similarity 42.1%; Pred. No. 32;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ILRGESLNKSLPILHEWK 20
Db 80 LITGSLRKNVPLHDAYF 98

RESULT 8
US-10-282-122A-60551
; Sequence 60551, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangseu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60551
; LENGTH: 768
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60551

Query Match 35.5%; Score 49; DB 4; Length 768;
Best Local Similarity 34.8%; Pred. No. 1.8e+02;
Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 NILRGESLNKSLPILHEWKFFDY 23
Db 540 NLKASQSVNKVLQVQYDWSADY 562

```

```
RESULT 9
US-10-437-963-106441
; Sequence 106441, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106441
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(152)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_10885C.1.pep
US-10-437-963-106441
Query Match 34.8%; Score 48; DB 4; Length 152;
Best Local Similarity 53.3%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 ESLNKSILPILHEWKF 20
Db 53 EPSKANLPLLHEWHF 67

RESULT 10
US-10-424-599-190654
; Sequence 190654, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190654
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_143180C.1.pep
US-10-424-599-190654
Query Match 34.8%; Score 48; DB 4; Length 439;
Best Local Similarity 52.6%; Pred. No. 1.5e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 5 GESLNKSLP--ILHEWKFF 21
Db 130 GESINSLPSPGSYKWKYY 148

RESULT 11
US-10-425-114-37354
; Sequence 37354, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37354
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: jC-gmle01810009c08_FLI.pep
US-10-425-114-37354
Query Match 34.8%; Score 48; DB 4; Length 445;
Best Local Similarity 52.6%; Pred. No. 1.5e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 5 GESLNKSLP--ILHEWKFF 21
Db 136 GESINSLPSPGSYKWKYY 154

RESULT 12
US-10-437-963-106443
; Sequence 106443, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106443
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_10887C.1.pep
US-10-437-963-106443
Query Match 34.8%; Score 48; DB 4; Length 541;
Best Local Similarity 53.3%; Pred. No. 1.8e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 ESLNKSILPILHEWKF 20
Db 321 EPSKANLPLLHEWHF 335

RESULT 13
US-10-032-585-7917
```


This Page Blank (12/20/20)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:12:24 ; Search time 1.44033 Seconds
(without alignments)
803.371 Million cell updates/sec

Title: US-10-525-567-2

Perfect score: 138

Sequence: 1 NILRGSLNKLSPILHEWKFDDYDF 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SID55/ptodata/1/pubpaa/US08 NEW PUB.pepl.*
- 2: /SID55/ptodata/1/pubpaa/US06 NEW PUB.pep.*
- 3: /SID55/ptodata/1/pubpaa/US07 NEW PUB.pep.*
- 4: /SID55/ptodata/1/pubpaa/US08 NEW PUB.pep.*
- 5: /SID55/ptodata/1/pubpaa/PCT NEW PUB.pep.*
- 6: /SID55/ptodata/1/pubpaa/US09 NEW PUB.pep.*
- 7: /SID55/ptodata/1/pubpaa/US09 NEW PUB.pep.*
- 8: /SID55/ptodata/1/pubpaa/US10 NEW PUB.pep.*
- 9: /SID55/ptodata/1/pubpaa/US10 NEW PUB.pep.*
- 10: /SID55/ptodata/1/pubpaa/US11 NEW PUB.pep.*
- 11: /SID55/ptodata/1/pubpaa/US11 NEW PUB.pep.*
- 12: /SID55/ptodata/1/pubpaa/US60 NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	35.5	768	11	US-11-045-004-2090
2	48	34.8	955	11	US-11-079-463-7834
3	47.5	34.4	204	11	US-11-009-658-40
4	46.5	33.7	444	11	US-11-072-512-2354
5	46	33.3	238	11	US-11-096-568A-33583
6	46	33.3	268	11	US-11-079-463-8150
7	46	33.3	314	11	US-11-096-568A-33582
8	46	33.3	334	11	US-11-096-568A-33581
9	45	32.6	135	11	US-11-096-568A-1311
10	45	32.6	538	11	US-11-087-099-1023
11	45	32.6	538	11	US-11-087-099-8465
12	45	32.6	538	11	US-11-087-099-11979
13	45	32.6	538	11	US-11-188-298-18858
14	44	31.9	201	11	US-11-188-298-18858
15	44	31.9	219	11	US-11-087-099-6165
16	44	31.9	240	11	US-11-179-977-19
17	44	31.9	260	11	US-11-096-568A-6893
18	44	31.9	305	9	US-10-063-703-108
19	44	31.9	305	9	US-10-194-487-324
20	44	31.9	305	9	US-10-195-883-324
21	44	31.9	305	9	US-10-195-888-324

Sequence 324, App
Sequence 108, App
Sequence 108, App
Sequence 4, Appli
Sequence 2, Appli
Sequence 8270, Ap
Sequence 17331, A
Sequence 1736, Ap
Sequence 1472, Ap
Sequence 10168, A
Sequence 102, App
Sequence 1745, Ap
Sequence 1746, Ap
Sequence 6, Appli
Sequence 7687, Ap
Sequence 1220, Ap
Sequence 5736, Ap
Sequence 8020, Ap
Sequence 12109, A
Sequence 11154, A
Sequence 12172, A
Sequence 16274, A
Sequence 18448, A
Sequence 4, Appli

US-10-195-889-324
US-11-102-240-108
US-11-103-195-108
US-11-022-490A-4
US-11-135-603-2
US-11-079-463-8270
US-11-188-298-17331
US-11-004-399-1736
US-10-821-234-1472
US-11-098-686-10168
US-11-052-554A-102
US-11-264-096-1745
US-11-264-096-1746
US-10-523-362-6
US-11-087-099-7687
US-11-087-099-1220
US-11-087-099-5736
US-11-087-099-8020
US-11-188-298-11154
US-11-188-298-12172
US-11-188-298-16274
US-11-188-298-18448
US-11-314-018-4

ALIGNMENTS

RESULT 1

US-11-045-004-2090
Sequence 2090, Application US/11045004
Publication No. US20060078901A1

GENERAL INFORMATION:
APPLICANT: BUCHRISE, CARMEN

APPLICANT: FRANGEUL, LIONEL

APPLICANT: COUVE, ELISABETH

APPLICANT: RUSNIOK, CHRISTOPHE

APPLICANT: FSIHI, HAFIDA

APPLICANT: DEHOIX, PIERRE

APPLICANT: DUSSURGET, OLIVIER

APPLICANT: CHETOUANI, FARID

APPLICANT: NEDJARI, HAFED

APPLICANT: GLASER, PHILIPPE

APPLICANT: KINST, FRANCK

APPLICANT: COSSART, PASCALE

APPLICANT: DANIELS, JUSTIN

APPLICANT: GOEBEL, WERNER

APPLICANT: KREFT, JURGEN

APPLICANT: KUHN, MICHAEL

APPLICANT: NG, EVA

APPLICANT: VAZQUEZ-BOLAND, ANTONIO

APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO

APPLICANT: GARRIDO-GARCIA, PATRICIA

APPLICANT: TIERREZ-MARTINEZ, ALBERTO

APPLICANT: AMEND, ALEXANDRA

APPLICANT: CHAKRABORTY, TRINAD

APPLICANT: DOMANN, EUGEN

APPLICANT: HAIN, THORSTEN

APPLICANT: BERCHE, PATRICK

APPLICANT: CHARBIT, ALAIN

APPLICANT: DURANT, LIONEL

APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO

APPLICANT: BAQUERO, FERNANDO

APPLICANT: GARCIA DEL PORTILLO, FRANCISCO

APPLICANT: GOMEZ-LOPEZ, NURIA

APPLICANT: MADUENIO, ENCARNIA

APPLICANT: PABLOS, BETRIZ DE

APPLICANT: WEHLAND, JURGEN

APPLICANT: KARST, UWE

APPLICANT: ENTIAN, KARL-DIETER

APPLICANT: HAUF, JORG

APPLICANT: ROSE, MATTHIAS

```

; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2090
; LENGTH: 768
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-2090

Query Match      35.5%; Score 49; DB 11; Length 768;
Best Local Similarity 34.8%; Pred. No. 13;
Matches 8; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 NLRGSLNKSILPILHEWKFFDY 23
   : : : : : : : : : : : : : : : :
Db 540 NLRASQSVNKLQVQVDSSADY 562

RESULT 2
US-11-079-463-7834
; Sequence 7834, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7834
; LENGTH: 955
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-7834

Query Match      34.8%; Score 48; DB 11; Length 955;
Best Local Similarity 53.3%; Pred. No. 24;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 RGSLSNKSILPILHEW 18
   : : : : : : : : : : : : : : :
Db 138 KDEALDRSLILHDW 152

RESULT 3
US-11-009-658-40
; Sequence 40, Application US/11009658
; Publication No. US2006003430A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Lysophosphatidic Acid Acetyltransferases
; FILE REFERENCE: BB1332
; CURRENT APPLICATION NUMBER: US/11/009,658
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US/09/914,098
; PRIOR FILING DATE: 2001-08-22

```

```

; PRIOR APPLICATION NUMBER: 60/121,119
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 40
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (68)
; OTHER INFORMATION: Xaa = any amino acid
US-11-009-658-40

Query Match      34.4%; Score 47.5; DB 11; Length 204;
Best Local Similarity 47.1%; Pred. No. 5.1;
Matches 8; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 7 SLNKSILPILHEWKFFDY 23
   : : : : : : : : : : : : : : :
Db 168 ALN-ALPTYYSWRFYDY 183

RESULT 4
US-11-072-512-2354
; Sequence 2354, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2354
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2354

Query Match      33.7%; Score 46.5; DB 11; Length 444;
Best Local Similarity 30.0%; Pred. No. 18;
Matches 12; Conservative 1; Mismatches 10; Indels 17; Gaps 1;

QY 3 LRGSLSL-----NKSILPILHEWKFFDYDF 25
   : : : : : : : : : : : : : : :
Db 60 IRGERLRDKWVLECMKKDLIYNKVTPTFFHWKIDDKKF 99

RESULT 5
US-11-096-568A-33583

```

```
; Sequence 33583, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33583
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(238)
; OTHER INFORMATION: Ceres Seq. ID no. 13603494
US-11-096-568A-33583

Query Match      33.3%; Score 46; DB 11; Length 238;
Best Local Similarity 43.8%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy      8 LNKSLPILHEWKFFDY 23
      : : ||| |
Db     34 IQRFLLPQQSWTFDY 49

RESULT 6
US-11-079-463-8150
; Sequence 8150, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 8150
; LENGTH: 268
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-8150

Query Match      33.3%; Score 46; DB 11; Length 268;
Best Local Similarity 38.9%; Pred. No. 12;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy      8 LNKSLPILHEWKFFDYDF 25
      || : ||| : ||| :
Db     186 LNRHTGKIAEWKMYDNY 203

RESULT 7
US-11-096-568A-33582
; Sequence 33582, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33582
```

```
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(314)
; OTHER INFORMATION: Ceres Seq. ID no. 13603493
US-11-096-568A-33582

Query Match      33.3%; Score 46; DB 11; Length 314;
Best Local Similarity 43.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy      8 LNKSLPILHEWKFFDY 23
      : : ||| |
Db     110 IQRFLLPQQSWTFDY 125

RESULT 8
US-11-096-568A-33581
; Sequence 33581, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33581
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(334)
; OTHER INFORMATION: Ceres Seq. ID no. 13603492
US-11-096-568A-33581

Query Match      33.3%; Score 46; DB 11; Length 334;
Best Local Similarity 43.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy      8 LNKSLPILHEWKFFDY 23
      : : ||| |
Db     130 IQRFLLPQQSWTFDY 145

RESULT 9
US-11-096-568A-1311
; Sequence 1311, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1311
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(135)
; OTHER INFORMATION: Ceres Seq. ID no. 14302141
US-11-096-568A-1311

Query Match      32.6%; Score 45; DB 11; Length 135;
Best Local Similarity 46.7%; Pred. No. 8.1;
```

```
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 5 GESLNKSLPILHEWK 19
    | : | : | : | : |
Db 28 GITLRQHPIPIFHHK 42

RESULT 10
US-11-087-099-1023
; Sequence 1023, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1023
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Candida maltosa
US-11-087-099-1023

Query Match 32.6%; Score 45; DB 11; Length 538;
Best Local Similarity 45.5%; Pred. No. 37;
Matches 10; Conservative 3; Mismatches 7; Indels 2; Gaps 1;
QY 2 ILRGESLNKSLPILHEWKFFDY 23
    ||| ||| : ||| :
Db 270 ILNGSKFNKSIKTVH--KPADF 289

RESULT 11
US-11-087-099-8465
; Sequence 8465, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8465
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Candida maltosa
US-11-087-099-8465

Query Match 32.6%; Score 45; DB 11; Length 538;
Best Local Similarity 45.5%; Pred. No. 37;
Matches 10; Conservative 3; Mismatches 7; Indels 2; Gaps 1;
QY 2 ILRGESLNKSLPILHEWKFFDY 23
    ||| ||| : ||| :
Db 270 ILNGSKFNKSIKTVH--KPADF 289

RESULT 12
US-11-188-298-11979
; Sequence 11979, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 11979
```

```
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Candida maltosa
US-11-188-298-11979

Query Match 32.6%; Score 45; DB 11; Length 538;
Best Local Similarity 45.5%; Pred. No. 37;
Matches 10; Conservative 3; Mismatches 7; Indels 2; Gaps 1;
QY 2 ILRGESLNKSLPILHEWKFFDY 23
    ||| ||| : ||| :
Db 270 ILNGSKFNKSIKTVH--KPADF 289

RESULT 13
US-11-188-298-18858
; Sequence 18858, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 18858
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Candida maltosa
US-11-188-298-18858

Query Match 32.6%; Score 45; DB 11; Length 538;
Best Local Similarity 45.5%; Pred. No. 37;
Matches 10; Conservative 3; Mismatches 7; Indels 2; Gaps 1;
QY 2 ILRGESLNKSLPILHEWKFFDY 23
    ||| ||| : ||| :
Db 270 ILNGSKFNKSIKTVH--KPADF 289

RESULT 14
US-11-096-568A-6894
; Sequence 6894, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6894
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(201)
; OTHER INFORMATION: Ceres Seq. ID no. 15168590
US-11-096-568A-6894

Query Match 31.9%; Score 44; DB 11; Length 201;
Best Local Similarity 39.1%; Pred. No. 18;
Matches 9; Conservative 2; Mismatches 12; Indels 0; Gaps 0;
QY 3 LRGESLNKSLPILHEWKFFDYDF 25
    ||| ||| : ||| :
Db 146 LRGFDLNLPAPLTFEWSPMGFDF 168
```

Thu May 4 17:23:16 2006

```
RESULT 15
US-11-087-099-6165
; Sequence 6165, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6165
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Nicotiana glauca
US-11-087-099-6165

Query Match      31.9%; Score 44; DB 11; Length 219;
Best Local Similarity 39.1%; Pred. No. 20;
Matches 9; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

Qy      1 NILGESLNKSLPILHEWKPFYD 23
Db      188 NCMENERVSKSLP--HPHKIYDP 208

Search completed: May 3, 2006, 19:18:56
Job time : 3.44033 secs
```

This Page Blank (usps)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 18:53:48 ; Search time 222.646 Seconds
(without alignments)
1034.083 Million cell updates/sec

Title: US-10-525-567-3
Perfect score: 2796
Sequence: 1 AAVNQRKSNLAHSMKVI.....NNQNDNRNDNQVHHSSKLH 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2796	100.0	524	8	ADL27606 Honey bee
2	2796	100.0	544	8	ADL27616 Honey bee
3	2773	99.2	544	8	ADL27618 Honey bee
4	1420.5	50.8	414	8	ADL27617 Honey bee
5	1415.5	50.6	413	8	ADL27607 Honey bee
6	1415.5	50.6	432	4	AAQ78710 Oxygen pr
7	1415.5	50.6	432	4	AAQ78815 Bee prote
8	1415.5	50.6	432	8	ADL27619 Honey bee
9	427	15.3	541	4	ABB60127 Drosophil
10	422.5	15.1	426	4	ABB66147 Drosophil
11	416.5	15.0	453	4	ABB71124 Drosophil
12	415.5	14.9	412	4	ABB64733 Drosophil
13	408.5	14.6	415	4	ABB64727 Drosophil
14	408.5	14.6	438	4	ABB60071 Drosophil
15	322.5	11.5	256	2	AAQ24796 Sequence
16	320	11.4	429	4	ABB67082 Drosophil
17	319.5	11.4	409	4	ABB66148 Drosophil
18	313.5	11.2	342	2	AAW03625 Human lut
19	302.5	10.8	379	4	ABB71640 Drosophil
20	294.5	10.5	316	4	ABB58294 Drosophil
21	290	10.4	590	2	AAQ11019 Apo-lipop
22	289.5	10.4	293	9	AEB40378 L. pneumo
23	282.5	10.1	319	9	AEB37025 L. pneumo
24	281	10.1	530	4	ABB71802 Drosophil

25	267	9.5	2150	5	AAO22566	Aao22566 Wooden le
26	261	9.3	190	2	AAQ41992	Aar41992 Staphyloc
27	261	9.3	1712	3	AAQ18205	Aab18205 Plasmodiu
28	260	9.3	190	2	AAQ42004	Aar42004 Staphyloc
29	258	9.2	190	2	AAQ41996	Aar41996 Staphyloc
30	258	9.2	190	2	AAQ42012	Aar42012 Staphyloc
31	258	9.2	190	2	AAQ41995	Aar41995 Staphyloc
32	257	9.2	190	2	AAQ42011	Aar42011 Staphyloc
33	257	9.2	190	2	AAQ41994	Aar41994 Staphyloc
34	257	9.2	190	2	AAQ42010	Aar42010 Staphyloc
35	256	9.2	190	2	AAQ41998	Aar41998 Staphyloc
36	256	9.2	190	2	AAQ42002	Aar42002 Staphyloc
37	256	9.2	190	2	AAQ41989	Aar41989 Staphyloc
38	256	9.2	190	2	AAQ41993	Aar41993 Staphyloc
39	256	9.2	190	2	AAQ41991	Aar41991 Staphyloc
40	256	9.2	190	2	AAQ41997	Aar41997 Staphyloc
41	256	9.2	190	2	AAQ42003	Aar42003 Staphyloc
42	255	9.1	190	2	AAQ41990	Aar41990 Staphyloc
43	255	9.1	190	2	AAQ41999	Aar41999 Staphyloc
44	255	9.1	190	2	AAQ42013	Aar42013 Staphyloc
45	255	9.1	190	2	AAQ42005	Aar42005 Staphyloc

ALIGNMENTS

RESULT 1
ADL27606
ID ADL27606 standard; protein; 524 AA.
XX
AC ADL27606;
XX
DT 03-JUN-2004 (first entry)
XX
DE Honey bee RJP70 mature protein, SEQ ID 3.
XX
KW Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
KW royal jelly protein; allergy; pollinosis; atopic dermatitis;
KW contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP70.
XX
OS Apis mellifera.
XX
PN WO2004019971-A1.
XX
PD 11-MAR-2004.
XX
PF 26-AUG-2003; 2003WO-JP010795.
XX
PR 29-AUG-2002; 2002JP-00252087.
XX
PR 30-JAN-2003; 2003JP-00022776.
XX
(HAYA/) HAYASHIBARA K.
XX
Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;
WPI; 2004-248191/23.
DR N-FSDB; ADL27608.
XX
Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,
atopic dermatitis, contact hypersensitivity, bronchial asthma and
allergic rhinitis, comprise protein originated from royal jelly.
XX
Claim 1; SEQ ID NO 3; 78pp; Japanese.
XX
The present invention relates to novel antiallergic agents, which
comprise as an active ingredient, peptides ADL27604 and ADL27605, which
are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606
and ADL27607). The agents can be used to relieve symptoms accompanying an
allergic disease e.g. pollinosis, atopic dermatitis, contact
hypersensitivity, bronchial asthma and allergic rhinitis, which are
applicable in foods, cosmetics and drugs.
XX
Sequence 524 AA;

```
Query Match      100.0%; Score 2796; DB 8; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.e-219;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVNHQKSAANLAHSMKVIYEWKHIDDFGSDERRDAAIKSGEFDDHTKYPDFDVRWRD 60
DB 1 AAVNHQKSAANLAHSMKVIYEWKHIDDFGSDERRDAAIKSGEFDDHTKYPDFDVRWRD 60
QY 61 KTFVTIERNNGVPSLLNVVTKKGGPGLLRPPYDMSFAKYEDCSGIVSAFKIAVDKFR 120
DB 61 KTFVTIERNNGVPSLLNVVTKKGGPGLLRPPYDMSFAKYEDCSGIVSAFKIAVDKFR 120
QY 121 LWVLDSGLVNNQPMCSPKLLTFDLKTSKLVKQVEIPHNIAVNATTGMGELVSLAVQAID 180
DB 121 LWVLDSGLVNNQPMCSPKLLTFDLKTSKLVKQVEIPHNIAVNATTGMGELVSLAVQAID 180
QY 181 RTNTMVIADKEGGLIMYQNSDDSPHRLTSNTFDYDPRYTKLTVAGESFTVKNKGCIA 240
DB 181 RTNTMVIADKEGGLIMYQNSDDSPHRLTSNTFDYDPRYTKLTVAGESFTVKNKGCIA 240
QY 241 LSPVTNNLYYSPSSHGLYYVDTEQFRNPQYEEENNVOYEGSQDILNTQSFQKVVSKNGVL 300
DB 241 LSPVTNNLYYSPSSHGLYYVDTEQFRNPQYEEENNVOYEGSQDILNTQSFQKVVSKNGVL 300
QY 301 FLGLVNGSGIACVNEHQVLORESFDVVAQNEETLQIMVSMKIMENLPQSGRINDPEGNEY 360
DB 301 FLGLVNGSGIACVNEHQVLORESFDVVAQNEETLQIMVSMKIMENLPQSGRINDPEGNEY 360
QY 361 MLALSNRMQKIINDDFNFDVNFRIILGANVDDLMRNTRCGRYHYNQAGNQADNQADNQ 420
DB 361 MLALSNRMQKIINDDFNFDVNFRIILGANVDDLMRNTRCGRYHYNQAGNQADNQADNQ 420
QY 421 NANNQADNQANQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 480
DB 421 NANNQADNQANQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 480
QY 481 NDNKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 524
DB 481 NDNKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 524

RESULT 2
ADL27616
ID ADL27616 standard; protein; 544 AA.
AC ADL27616;
XX ADL27616;
XX ADL27616;
DE 03-JUN-2004 (first entry)
XX Honey bee RJP70.
XX Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
XX royal jelly protein; allergy; pollinosis; atopic dermatitis;
XX contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP70.
XX
XX Apis mellifera.
XX
XX Key Location/Qualifiers
XX Peptide 1-20
XX /label= Signal_peptide
XX Protein 21..544
XX /label= Mature_protein
XX
XX WO2004019971-A1.
XX
XX 11-MAR-2004.
XX
XX 26-AUG-2003; 2003WO-JP010795.
XX
XX 29-AUG-2002; 2002JP-00252087.
XX
XX 30-JAN-2003; 2003JP-00022776.
XX
```

```
PA (HAYA/) HAYASHIBARA K.
XX Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;
XX WPI; 2004-248191/23.
DR N-PSDB; ADL27608.
XX Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,
PT atopic dermatitis, contact hypersensitivity, bronchial asthma and
PT allergic rhinitis, comprise protein originated from royal jelly.
XX
PS Disclosure; Page 59-62; 78pp; Japanese.
XX
CC The present invention relates to novel antiallergic agents, which
CC comprise as an active ingredient, peptides ADL27604 and ADL27605, which
CC are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606
CC and ADL27607). The agents can be used to relieve symptoms accompanying an
CC allergic disease e.g. pollinosis, atopic dermatitis, contact
CC hypersensitivity, bronchial asthma and allergic rhinitis, which are
CC applicable in foods, cosmetics and drugs. The present sequence is a honey
CC bee RJP.
XX
SQ Sequence 544 AA;
Query Match      100.0%; Score 2796; DB 8; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.e-219;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAVNHQKSAANLAHSMKVIYEWKHIDDFGSDERRDAAIKSGEFDDHTKYPDFDVRWRD 60
DB 21 AAVNHQKSAANLAHSMKVIYEWKHIDDFGSDERRDAAIKSGEFDDHTKYPDFDVRWRD 80
QY 61 KTFVTIERNNGVPSLLNVVTKKGGPGLLRPPYDMSFAKYEDCSGIVSAFKIAVDKFR 120
DB 81 KTFVTIERNNGVPSLLNVVTKKGGPGLLRPPYDMSFAKYEDCSGIVSAFKIAVDKFR 140
QY 121 LWVLDSGLVNNQPMCSPKLLTFDLKTSKLVKQVEIPHNIAVNATTGMGELVSLAVQAID 180
DB 141 LWVLDSGLVNNQPMCSPKLLTFDLKTSKLVKQVEIPHNIAVNATTGMGELVSLAVQAID 200
QY 181 RTNTMVIADKEGGLIMYQNSDDSPHRLTSNTFDYDPRYTKLTVAGESFTVKNKGCIA 240
DB 201 RTNTMVIADKEGGLIMYQNSDDSPHRLTSNTFDYDPRYTKLTVAGESFTVKNKGCIA 260
QY 241 LSPVTNNLYYSPSSHGLYYVDTEQFRNPQYEEENNVOYEGSQDILNTQSFQKVVSKNGVL 300
DB 261 LSPVTNNLYYSPSSHGLYYVDTEQFRNPQYEEENNVOYEGSQDILNTQSFQKVVSKNGVL 320
QY 301 FLGLVNGSGIACVNEHQVLORESFDVVAQNEETLQIMVSMKIMENLPQSGRINDPEGNEY 360
DB 321 FLGLVNGSGIACVNEHQVLORESFDVVAQNEETLQIMVSMKIMENLPQSGRINDPEGNEY 380
QY 361 MLALSNRMQKIINDDFNFDVNFRIILGANVDDLMRNTRCGRYHYNQAGNQADNQADNQ 420
DB 381 MLALSNRMQKIINDDFNFDVNFRIILGANVDDLMRNTRCGRYHYNQAGNQADNQADNQ 440
QY 421 NANNQADNQANQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 480
DB 441 NANNQADNQANQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 500
QY 481 NDNKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 524
DB 501 NDNKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 544

RESULT 3
ADL27618
ID ADL27618 standard; protein; 544 AA.
XX ADL27618;
XX ADL27618;
DT 03-JUN-2004 (first entry)
XX
```

DE Honey bee MRJP3.

XX Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;

KW royal jelly protein; allergy; pollinosis; atopic dermatitis;

KW contact hypersensitivity; bronchial asthma; allergic rhinitis; MRJP3.

XX

XX Apis mellifera.

OS

XX

XX Key Location/Qualifiers

FT Peptide 1..16

FT Protein /label= Signal_peptide

FT Protein 17..544

FT Protein /label= Mature_protein

XX

XX WO2004019971-A1.

XX

XX 11-MAR-2004.

XX

XX 26-AUG-2003; 2003WO-JP010795.

XX

XX 29-AUG-2002; 2002JP-00252087.

PR 30-JAN-2003; 2003JP-00022776.

XX

XX (HAYA/) HAYASHIBARA K.

XX

XX Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;

PI

XX WPI; 2004-248191/23.

XX N-PSDB; ADL27610.

XX

XX Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,

PT atopic dermatitis, contact hypersensitivity, bronchial asthma and

PT allergic rhinitis, comprise protein originated from royal jelly.

XX

XX Disclosure; Page 65-69; 78pp; Japanese.

PS

XX The present invention relates to novel antiallergic agents, which

CC comprise as an active ingredient, peptides ADL27604 and ADL27605, which

CC are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606

CC and ADL27607). The agents can be used to relieve symptoms accompanying an

CC allergic disease e.g. pollinosis, atopic dermatitis, contact

CC hypersensitivity, bronchial asthma and allergic rhinitis, which are

CC applicable in foods, cosmetics and drugs. The present sequence is a honey

CC bee major RJP.

XX

XX Sequence 544 AA;

Query Match 99.2%; Score 2773; DB 8; Length 544;

Best Local Similarity 99.4%; Pred. No. 8e-218;

Matches 521; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAVNHQKSAANLAHSMKVIYEWKHIDPFGSDERRDAAIKSGEFDHTKNTYFFDVRWRD 60

DB 21 AAVNHQKSAANLAHSMKVIYEWKHIDPFGSDERRDAAIKSGEFDHTKNTYFFDVRWRD 80

QY 61 KTFVTIERNNGVPSLVNVTNKKGGPLLRRPYDPWSPAKYEDCSGIVSAFKIAVDKEDR 120

DB 81 KTFVTIERNNGVPSLVNVTNKKGGPLLRRPYDPWSPAKYEDCSGIVSAFKIAVDKEDR 140

QY 121 LWVLDGLVNNQPCSKPLTDFDLTKSLVKQVEIPHNIANVATTGMLVSLAVQAID 180

DB 141 LWVLDGLVNNQPCSKPLTDFDLTKSLVKQVEIPHNIANVATTGMLVSLAVQAID 200

QY 181 RNTVMYIADKEGELIMYQNSDDSFHRLTSNTFDYDPRYTKLTIVAGESFTVKNGICGIA 240

DB 201 RNTVMYIADKEGELIMYQNSDDSFHRLTSNTFDYDPRYTKLTIVAGESFTVKNGIYGIA 260

QY 241 LSPVTNNLYYSPLSHGLYYVDTQFRNPQYENNVQVEGSDIILNTQSGFKVSKNGVL 300

DB 261 LSPVTNNLYYSPLSHGLYYVDTQFRNPQYENNVQVEGSDIILNTQSGFKVSKNGVL 320

QY 301 FLGLVNGSIACVNEHQVLORESFDVVAQNEETLQIVSMKIMENLPQSGRINDPEGNEY 360

DB 321 FLGLVNGSIACVNEHQVLORESFDVVAQNEETLQIVSMKIMENLPQSGRINDPEGNEY 380

QY 361 MLALSNRMOKIINNDFNFNDVNFRIILGANVDDLNRNTRCGRYHQNAGNQADNQADNQ 420

DB 381 MLALSNRMOKIINNDFNFNDVNFRIILGANVDDLNRNTRCGRYHQNAGNQADNQADNQ 440

QY 421 NANNQADNQANQKQNGRQNDNRQNDKQNGRQNDKQNGRQNDKQNGRQNGKQ 480

DB 441 NANNQADNQANQKQNGRQNDNRQNDKQNGRQNDKQNGRQNDKQNGRQNGKQ 500

QY 481 NDNKQNGRQNDKQNGRQNDNRQNDKQNGRQNDKQNGRQNDKQNGRQNDKQNGRQNGKQ 524

DB 501 NDNKQNGRQNDKQNGRQNDNRQNDKQNGRQNDKQNGRQNDKQNGRQNDKQNGRQNGKQ 544

RESULT 4

ADL27617

ID ADL27617 standard; protein; 414 AA.

XX

XX AC ADL27617;

XX

XX 03-JUN-2004 (first entry)

XX

XX Honey bee RJP55.

XX

XX Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;

KW royal jelly protein; allergy; pollinosis; atopic dermatitis;

KW contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP55.

XX

XX Apis mellifera.

XX

XX WO2004019971-A1.

XX

XX 11-MAR-2004.

XX

XX 26-AUG-2003; 2003WO-JP010795.

XX

XX 29-AUG-2002; 2002JP-00252087.

PR 30-JAN-2003; 2003JP-00022776.

XX

XX (HAYA/) HAYASHIBARA K.

XX

XX Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;

PI

XX WPI; 2004-248191/23.

XX N-PSDB; ADL27609.

XX

XX Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,

PT atopic dermatitis, contact hypersensitivity, bronchial asthma and

PT allergic rhinitis, comprise protein originated from royal jelly.

XX

XX Disclosure; Page 62-65; 78pp; Japanese.

PS

XX The present invention relates to novel antiallergic agents, which

CC comprise as an active ingredient, peptides ADL27604 and ADL27605, which

CC are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606

CC and ADL27607). The agents can be used to relieve symptoms accompanying an

CC allergic disease e.g. pollinosis, atopic dermatitis, contact

CC hypersensitivity, bronchial asthma and allergic rhinitis, which are

CC applicable in foods, cosmetics and drugs. The present sequence is a honey

CC bee RJP.

XX

XX Sequence 414 AA;

Query Match 50.8%; Score 1420.5; DB 8; Length 414;

Best Local Similarity 65.3%; Pred. No. 2.3e-107;

Matches 265; Conservative 63; Mismatches 65; Indels 13; Gaps 2;

QY 12 NLAHSMKVIYEWKHIDPFGSDERRDAAIKSGEFDHTKNTYFFDVRWRDFTVTIERNNG 71

DB 8 SLNKSPLTILHEWKFFDFGSDERRDAAIKSGEFDHTKNTYFFDVRWRDFTVTIERNNG 67

QY 72 VPSSLVNVTNKKGGPLLRRPYDPWSPAKYEDCSGIVSAFKIAVDKFDRLWVLDGLVNN 131


```

Query Match      50.6%; Score 1415.5; DB 4; Length 432;
Best Local Similarity 65.0%; Pred. No. 6.3e-107;
Matches 264; Conservative 63; Mismatches 66; Indels 13; Gaps 2;

QY 12 NLAHSMKVIYEWKHIDFDFGSDERRDAAIKSGFDHTKNTYPPDVRWRDKTFVTIERNNG 71
DB 26 SLNKSILPILHEWKFFDYDFGSDERRDAILSGEYDKNNYPSDIDQWHDKIFVTMLRYNG 85

QY 72 VPSSLNVVTKKGGPGLLRYPDPWSFAKYEDCSGIVSAFKIAVDKFDRLWLDGLVNN 131
DB 86 VPSSLNVISKVGDGGLLPQYPDPWSFAKYDDCSGIVSASKLAIDKCDRLWLDGLVNN 145

QY 132 NOPMCSPKLLTFDLTKSLVKQVEIPHNIAVNATTGMEGLVSLAVQAID--RTNTWYI 188
DB 146 TOPMCSPKLLTFDLTTSQLLKQVEIPHDAVNATTGKRLSSLAVALQSLDCNTNSDTWYI 205

QY 189 ADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRTYKLTWAGESFTVKGICGIALSPVTNNL 248
DB 206 ADEKGEGLIYVHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGVALSPMTNNL 265

QY 249 YYSPLSHGLYVYDTEQFRNPQYENNVQYEGSQDILNTQSGFKVSKNGVLFGLVGN 308
DB 266 YYSPLVASTSLYYNTQFRNTSDYQNDIHVEGVQNILDTQSSAKVSKGVLFPGLVGDS 325

QY 309 GIACVNEHVLQRESFDVVAQNEETLQIMVSKMIMENLPQSGRINDPEGNEYMLALNRM 368
DB 326 ALGCWNEHRLTHERNIRTVAQSDDELQMIASMKIKEAXPHVPIDRYINREYILVLSNKM 385

RESULT 7
AAG78815
ID AAG78815 standard; protein; 432 AA.
AC AAG78815;
XX
XX 27-NOV-2001 (first entry)
XX
XX Bee protein.
XX
XX Bee; lactic acid accumulation inhibitor; royal jelly; muscular fatigue.
XX
XX Apis mellifera.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX Protein /label= Signal_peptide
XX /label= Mature_bee_protein
XX Misc-difference 363
XX /label= unknown
XX /note= "Encoded by CTN, given as Xaa in specification"
XX
XX JP2001172190-A.
XX
XX 26-JUN-2001.
XX
XX 15-DEC-1999; 99JP-00356006.
XX
XX 15-DEC-1999; 99JP-00356006.
XX
XX (POKK ) POLA CHEM IND INC.
XX
XX WPI; 2001-592556/67.
XX N-PSDB; AAI65041.
XX
XX Lactic acid accumulation inhibitor comprises protein contained in royal
XX jelly, useful for restoration, improvement and release of muscular
XX fatigue.
XX

```

```

PS Disclosure; Page 9-10; 10pp; Japanese.
XX
XX The present invention relates to a lactic acid accumulation inhibitor.
XX The inhibitor comprises a protein contained in royal jelly having lactic
XX acid accumulation inhibiting activity as the active component. The lactic
XX acid accumulation inhibitor is used for restoration, improvement and
XX release of muscular fatigue. The present sequence is a bee protein, which
XX was used in the present invention
XX
XX Sequence 432 AA;
XX
Query Match      50.6%; Score 1415.5; DB 4; Length 432;
Best Local Similarity 65.0%; Pred. No. 6.3e-107;
Matches 264; Conservative 63; Mismatches 66; Indels 13; Gaps 2;

QY 12 NLAHSMKVIYEWKHIDFDFGSDERRDAAIKSGFDHTKNTYPPDVRWRDKTFVTIERNNG 71
DB 26 SLNKSILPILHEWKFFDYDFGSDERRDAILSGEYDKNNYPSDIDQWHDKIFVTMLRYNG 85

QY 72 VPSSLNVVTKKGGPGLLRYPDPWSFAKYEDCSGIVSAFKIAVDKFDRLWLDGLVNN 131
DB 86 VPSSLNVISKVGDGGLLPQYPDPWSFAKYDDCSGIVSASKLAIDKCDRLWLDGLVNN 145

QY 132 NOPMCSPKLLTFDLTKSLVKQVEIPHNIAVNATTGMEGLVSLAVQAID--RTNTWYI 188
DB 146 TOPMCSPKLLTFDLTTSQLLKQVEIPHDAVNATTGKRLSSLAVALQSLDCNTNSDTWYI 205

QY 189 ADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRTYKLTWAGESFTVKGICGIALSPVTNNL 248
DB 206 ADEKGEGLIYVHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGVALSPMTNNL 265

QY 249 YYSPLSHGLYVYDTEQFRNPQYENNVQYEGSQDILNTQSGFKVSKNGVLFGLVGN 308
DB 266 YYSPLVASTSLYYNTQFRNTSDYQNDIHVEGVQNILDTQSSAKVSKGVLFPGLVGDS 325

QY 309 GIACVNEHVLQRESFDVVAQNEETLQIMVSKMIMENLPQSGRINDPEGNEYMLALNRM 368
DB 326 ALGCWNEHRLTHERNIRTVAQSDDELQMIASMKIKEAXPHVPIDRYINREYILVLSNKM 385

QY 369 QKIINNDNFNDVNFRIILGANVDDLMRNTCRGRYHQNAGNQADN 414
DB 386 QKMVNDNFDDVNFRIIMNANVNELILNTRC-----ENPDN 421

RESULT 8
ADL27619
ID ADL27619 standard; protein; 432 AA.
XX
XX ADL27619;
XX
XX 03-JUN-2004 (first entry)
XX
XX Honey bee MRJP1.
XX
XX Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
XX royal jelly protein; allergy; pollinosis; atopic dermatitis;
XX contact hypersensitivity; bronchial asthma; allergic rhinitis; MRJP1.
XX
XX Apis mellifera.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX Protein /label= Signal_peptide
XX /label= Mature_protein
XX
XX WO2004019971-A1.
XX
XX 11-MAR-2004.
XX
XX 26-AUG-2003; 2003WO-JP010795.
XX
XX 29-AUG-2002; 2002JP-00252087.
XX

```


AC	ABB66147;	
XX	26-MAR-2002 (first entry)	
DT	Drosophila melanogaster polypeptide SEQ ID NO 25233.	
DE	Drosophila; developmental biology; cell signalling; insecticide;	
DE	pharmaceutical.	
KW	Drosophila melanogaster.	
KW	WO200171042-A2.	
XX	27-SEP-2001.	
XX	23-MAR-2001; 2001WO-US009231.	
XX	23-MAR-2000; 2000US-0191637P.	
XX	11-JUL-2000; 2000US-00614150.	
XX	(PEKE) PE CORP NY.	
XX	Venter JC, Adams M, Li PWD, Myers EW;	
XX	WPI; 2001-656860/75.	
DR	N-PSDB; ABL10250.	
XX	New isolated nucleic acid detection reagent for detecting 1000 or more	
XX	genes from Drosophila and for elucidating cell signaling and cell-cell	
XX	interactions.	
XX	Disclosure; SEQ ID NO 25233; 2lpp + Sequence Listing; English.	
XX	The invention relates to an isolated nucleic acid detection reagent	
XX	capable of detecting 1000 or more genes from Drosophila. The invention is	
XX	useful in developmental biology and in elucidating cell signalling and	
XX	cell-cell interactions in higher eukaryotes for the development of	
XX	insecticides, therapeutics and pharmaceutical drugs. The invention	
XX	discloses genomic DNA sequences (AB16176-ABL30511), expressed DNA	
XX	sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-	
XX	ABB72072). The sequence data for this patent did not form part of the	
XX	printed specification, but was obtained in electronic format directly	
XX	from WIPO at ftp.wipo.int/pub/published_pct_sequences	
XX	Sequence 426 AA;	
QY	Query Match 15.1%; Score 422.5; DB 4; Length 426;	
DB	Best Local Similarity 26.2%; Pred. No. 1e-25;	
DB	Matches 111; Conservative 83; Mismatches 155; Indels 75; Gaps 13;	
QY	19 VIYWKHIDPFGSDERRDAIAKSGEFHTKXYPFVDWR-----RDKTFTVIER-NNG 71	
DB	34 IVFEMKQLQYFPSEQRDQVLRNGRNPDPSPIDIDVYPPNGGPPRHFTVTSFRFGQ 93	
QY	72 VPSSLNVTKKGGGLLRYP--DWSFAKVEDCSGIVSAFKAVKDFDLWLDSGLV 129	
DB	94 VPFSLGYTVNQRENGSIOAYPSYQMSHGANGDLTYSYRVHIDACGMWVLDSEI 153	
QY	130 NNNQPMCSPKLLTFDLKTSKLVQVEIPHNIAVNATTGMGLVSLAVQAIDR-----TN 183	
DB	154 EFVQ-HCAQVQVWFPLATDQLIHRYLPE---TSYKAKVSFVNIADIRPPSGQCKD 209	
QY	184 TWVIADKSGELIYQNSDPSFRLTNTFDY-DPRYTKLTVAGESFTVKNIGCIALS 242	
DB	210 VFAYLADTSAIVYDVVGQSMRI-ENKFTYPAKFGTHTVAGESFELLDGPLALATT 268	
QY	243 P-----VTNNLYSPSSHGLYVDTEQFNQYENNVQYEGSQDILNT----- 287	
DB	269 PLGLGLRRHLIFHALS-----NELELAIPDLILNATNWKQGLSSS 309	
QY	288 -----QSGKGVSKNGVFLGLVGNNGIACVNEHQVLORESFDVVVAQNEETLQ 335	
DB	310 LSEFTVLGKRGICQASHAISROGFLFCGFLPEIGFGWDIRRPYNNVKNLAINPATLQ 369	

QY	336 MIVSMKIMENLPQSGRINDPEGNEVYMLALSNRMQKIINDFNFDVNFRIILGANVDDLMR 395
DB	370 FVSGMKIVRR-PADGR-----EELWLLSDRLQKIFAGTIDYREINRVMRCDVDDLLQ 421
QY	396 NTRC 399
DB	422 GRGC 425

RESULT 11

ABB71124

ID ABB71124 standard; protein; 453 AA.

XX ABB71124;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 40164.

DE Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

KW Drosophila melanogaster.

OS WO200171042-A2.

PN 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL15227.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signaling and cell-cell

XX interactions.

XX Disclosure; SEQ ID NO 40164; 2lpp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

XX capable of detecting 1000 or more genes from Drosophila. The invention is

XX useful in developmental biology and in elucidating cell signalling and

XX cell-cell interactions in higher eukaryotes for the development of

XX insecticides, therapeutics and pharmaceutical drugs. The invention

XX discloses genomic DNA sequences (AB16176-ABL30511), expressed DNA

XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-

XX ABB72072). The sequence data for this patent did not form part of the

XX printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 453 AA;

QY Query Match 15.0%; Score 418.5; DB 4; Length 453;

DB Best Local Similarity 27.9%; Pred. No. 2.4e-25;

DB Matches 122; Conservative 84; Mismatches 194; Indels 37; Gaps 12;

QY 16 SMKVIYWKHIDPFGSDERRDAIAKSGEFHTKXYPFVDWRDKTFTVIER-NNGVPS 74

DB 21 NLRVAYEWREMDFKYANPDQKWSAIERGEKPAKVPIFGLEVAGHRLFTVTLPRWRDGVPA 80

QY 75 SLNVV-TNKKGGGFLRPPYPDWSFAKVEDCS-CIVSAFKIADVDFDLWLVD---SGLV 129

DB 81 SLAYLDLNDTSSKGFALKPFPSWQAHNLQEAPELVSFPRVADRCCGRLWLDSRISGLV 140

QY 130 NNNQPMCSPKLLTFDLKTSKLVQVEIPHNIAVNATTGMGLVSLAVQAIDRTNTMYIA 189

Db	141	EQTKIVGAQLLYDHLNDDLLRRHVLPAQOLKQGSLL-----LANLAVEDSDCENTFAYAA	196
Qy	190	DERGEGIMTQNSDDSFHRLTSNTFDYDPRYTKLTAVAGESFTVKNGIGICIALS-PVTN--	246
Db	197	DLGSPGLVVSXKDEESWRVQHFFHDPDPWAGNFSINGIEFQWDDGGLGLALSKELETGY	256
Qy	247	-NLYSPLSHGLYYVDTEQFRNPQVEENNVOYE-----GSQDILNTQSGKVVSKN-GV	299
Db	257	ATLYFHLPLCSTTFBSVDTSLRNKTLATSPMIREFKVLGSRG-PNTQAGABFLDPTGV	315
Qy	300	LELGLVNSGIACVNEHVLQRESFDVVAQBEETLQMVSMKIMENLPQSGRINDEPENE	359
Db	316	LFYALPNLNEVACWRTATDSHSSQSQRHNNDTLVFPSPDIKV-----DDQK	362
Qy	360	YMLALSNRMKIINNDFNFDVNFRIILGANVDDLMRTRCGRYHNNQVAGNQADNQNADN	419
Db	363	RLWVLSNQLPVFIYDELYAGSINFRILITASVKEAIENTAC---EIRTSPLPDVINKLGD	419
Qy	420	QNANNQVADNQNANKON	436
Db	420	LNTNKLKSNASSLRN	436
RESULT 12			
ABBE64733			
ID	ABBE64733	standard; protein; 412 AA.	
AC	ABBE64733;		
DT	26-MAR-2002	(first entry)	
XX	Drosophila melanogaster polypeptide SEQ ID NO 20991.		
XX	Drosophila; developmental biology; cell signalling; insecticide;		
XX	pharmaceutical.		
OS	Drosophila melanogaster.		
PN	WO200171042-A2.		
XX	27-SEP-2001.		
XX	23-MAR-2001;	2001WO-US009231.	
PR	23-MAR-2000;	2000US-0191637P.	
PR	11-JUL-2000;	2000US-00614150.	
XX	(PEKE)	PE CORP NY.	
PA	Venter JC, Adams M, Li PWD, Myers EW;		
XX	WPI; 2001-656860/75.		
DR	N-PSDB; ABL08836.		
XX	New isolated nucleic acid detection reagent for detecting 1000 or more		
PT	genes from Drosophila and for elucidating cell signalling and cell-cell		
PT	interactions.		
XX	Disclosure; SEQ ID NO 20991; 21pp + Sequence Listing; English.		
XX	The invention relates to an isolated nucleic acid detection reagent		
CC	capable of detecting 1000 or more genes from Drosophila. The invention is		
CC	useful in developmental biology and in elucidating cell signalling and		
CC	cell-cell interactions in higher eukaryotes for the development of		
CC	insecticides, therapeutics and pharmaceutical drugs. The invention		
CC	discloses genomic DNA sequences (ABU16176-ABU130511), expressed DNA		
CC	sequences (ABU01840-ABU16175) and the encoded proteins (ABBS7737-		
CC	ABBS72072). The sequence data for this patent did not form part of the		
CC	printed specification, but was obtained in electronic format directly		
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences		
XX	Sequence 412 AA;		
, SQ			
Query Match 14.9%; Score 415.5; DB 4; Length 412;			
Best Local Similarity 28.7%; Pred. No. 3.7e-25;			
Matches 117; Conservative 80; Mismatches 174; Indels 37; Gaps 14;			
Qy	14	AHSMKVIYEWKHIDPFGSDERRDAIKSGEPDHTKNYPFDVD--RWRDKT---FVTIE	67
Db	19	AQALSVFGAYNLELEFPSPQERQALRDGLYDPGSVIPIDVDVYKKGDATPSIFVTIP	78
Qy	68	R-NNGVPSLNVVTKKGGPPLREYP--DWSFAKYEDCSGIVSAFKIADVDFDLWL	124
Db	79	RFAGKVPYSLAYVTVNMRPNTLLQAYPSYWHKSHGADCNGLTSVYRTQIDCGRMWIL	138
Qy	125	DSGLVNNQPMGCPKLLTDFDLTKTSKLVQVEIPHNTAVNATTGMGELVSLVAQAI	184
Db	139	DSGEIDFIQ-HCPPQLYALDESCKVAHQYKMPKRL---YKSGVSFRVPTVE-LDPHNC	193
Qy	185	---MVIADKCGELIMYQNSDDSFHRLTSNTFDY-DPRYTKLTAVAGESFTVKNGICGIA	240
Db	194	DVGFTVMADSIGDIVVYDVAAQSWRI-ENKFTYPHDPFGFTTIAGESFQLMDGT	252
Qy	241	LSP----VTNNLYSPLSHGLYYVDTEQFRN-POYEENNVQYEGSQDIL-----NTQSG	291
Db	253	LTPHGLGRRMYFHSLSSEWQMAIPLDVVNGSNWRLNDVSAALDQFOLLGKRGSCVA	312
Qy	292	KVVSNGVLFGLVNGSGIACVNEHVLQRESFDVVAQBEETLQMVSMKIMENLPQSGR	351
Db	313	AAMSESGFLTCGLVQVAPASLLANIRTGYSHONLMLVLEDEQRLQFASGLKIVRN-----	366
Qy	352	INDPEGNEYMLALSNEWMOKIINNDFNFDVNFRIILGANVDDLMRTRC	399
Db	367	---HEGKEELVLSNRLQKAFAGLDYKEINFRIQKGVQELLSGRPC	411
RESULT 13			
ABBE64727			
ID	ABBE64727	standard; protein; 415 AA.	
AC	ABBE64727;		
XX	26-MAR-2002	(first entry)	
XX	Drosophila melanogaster polypeptide SEQ ID NO 20973.		
XX	Drosophila; developmental biology; cell signalling; insecticide;		
XX	pharmaceutical.		
OS	Drosophila melanogaster.		
PN	WO200171042-A2.		
XX	27-SEP-2001.		
XX	23-MAR-2001;	2001WO-US009231.	
PR	23-MAR-2000;	2000US-0191637P.	
PR	11-JUL-2000;	2000US-00614150.	
XX	(PEKE)	PE CORP NY.	
PA	Venter JC, Adams M, Li PWD, Myers EW;		
XX	WPI; 2001-656860/75.		
DR	N-PSDB; ABL08830.		
XX	New isolated nucleic acid detection reagent for detecting 1000 or more		
PT	genes from Drosophila and for elucidating cell signalling and cell-cell		
PT	interactions.		
XX	Disclosure; SEQ ID NO 20973; 21pp + Sequence Listing; English.		
XX	The invention relates to an isolated nucleic acid detection reagent		
CC	capable of detecting 1000 or more genes from Drosophila. The invention is		
CC	useful in developmental biology and for elucidating cell signalling and		
CC	cell-cell interactions in higher eukaryotes for the development of		
CC	insecticides, therapeutics and pharmaceutical drugs. The invention		
CC	discloses genomic DNA sequences (ABU16176-ABU130511), expressed DNA		
CC	sequences (ABU01840-ABU16175) and the encoded proteins (ABBS7737-		
CC	ABBS72072). The sequence data for this patent did not form part of the		
CC	printed specification, but was obtained in electronic format directly		
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences		
XX	Sequence 412 AA;		

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:01:48 ; Search time 39.3539 Seconds
(without alignments)
1281.133 Million cell updates/sec

Title: US-10-525-567-3

Perfect score: 2796

Sequence: 1 AAVNHQKSAANLAHSMKVI.....NNQNDNRNDNQVHHSSKLH 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2269	81.2	467	2 S39193	royal jelly protei
2	1347	48.2	464	2 S39194	royal jelly protei
3	427	15.3	541	2 A25696	yellow protein - f
4	418.5	15.0	453	2 JG7253	Yellow-B protein -
5	278.5	10.0	3848	2 T17414	TipC protein - ali
6	267	9.5	2150	2 S71629	sensory transducti
7	261	9.3	1712	2 C71618	hypothetical prote
8	251	9.0	2819	2 T09080	probable chloroqui
9	247	8.8	568	2 JG7210	molluscan shell ma
10	247	8.8	1584	2 T18276	protein-tyrosine k
11	241	8.6	448	2 S05355	hypothetical prote
12	239.5	8.6	518	2 S23692	erythrocyte membra
13	236.5	8.5	1390	2 T14004	trfa protein - ali
14	227.5	8.1	4550	2 T18440	hypothetical prote
15	226.5	8.1	451	2 A23535	clustered asparagi
16	223.5	8.0	2452	1 RNZQ2L	DNA-directed RNA p
17	222.5	8.0	1650	2 T18444	hypothetical prote
18	222	7.9	1711	2 T18429	hypothetical prote
19	221.5	7.9	719	2 S61046	ARPI protein - yea
20	220	7.9	954	1 S20907	endo-1,4-beta-xyla
21	219.5	7.9	1093	2 T18275	1-phosphatidylinos
22	218.5	7.8	234	2 S14469	asparagine-rich pr
23	218.5	7.8	1817	2 D71606	hypothetical prote
24	217.5	7.8	537	2 A23770	asparagine-rich pr
25	217.5	7.8	3394	2 T18501	hypothetical prote
26	217	7.8	720	2 T51007	hypothetical prote
27	215.5	7.7	2457	2 T18492	hypothetical prote
28	215	7.7	3844	2 T18402	asparagine/asparta
29	212.5	7.6	725	2 T03219	G-quartet DNA bind

30	210	7.5	2500	2 G71609	hypothetical prote
31	209	7.5	839	2 H90577	lipoprotein vsai f
32	209	7.5	1256	2 S14556	asparagine-rich pr
33	208.5	7.5	1619	2 T18499	hypothetical prote
34	207	7.4	431	2 S50977	hypothetical prote
35	206.5	7.4	947	2 T08605	hypothetical prote
36	206.5	7.4	964	2 S48405	probable membrane
37	205.5	7.3	1254	2 T18277	kinesin heavy chai
38	201.5	7.2	1188	2 A71621	protein with 5'-3,
39	201	7.2	490	2 A46391	CAMP receptor subt
40	199.5	7.1	1278	2 A71609	probable secreted
41	199	7.1	608	2 T18437	hypothetical prote
42	196.5	7.0	1844	2 D71612	hypothetical prote
43	196	7.0	686	2 A71607	Mtn3/RAGLIP-like p
44	193.5	6.9	239	2 S14470	asparagine-rich pr
45	193	6.9	2391	2 T18410	carbamoyl-phosphat

ALIGNMENTS

RESULT 1

S39193

royal jelly protein RJP57-1 - honeybee

C;Species: Apis mellifera (honeybee)

C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 12-May-1995

C;Accession: S39193

R;Klaudiny, J.; Hanes, J.; Kulifajova, J.; Albert, S.; Simuth, J.

A;Submitted to the EMBL Data Library, September 1993

A;Description: Molecular cloning of two cDNAs from the head of the nurse honey bee (Apis

A;Reference number: S39193

A;Accession: S39193

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-467 <KLA>

A;Cross-references: UNIPARC:UPI0000179A48; EMBL:Z26318

Query Match 81.2%; Score 2269; DB 2; Length 467;
Best Local Similarity 96.9%; Pred. No. 2.7e-142;
Matches 435; Conservative 1; Mismatches 11; Indels 2; Gaps 2;

Qy	1	AAVNHQKSAANLAHSMKVIYEWKHIDFDGSDRRDAAIKSGBFDTKNTYPPFDVDRWD	60
Db	21	AAVNHQKSAANLAHSMKVIYEWKHIDFDGSDREMLRLNL-RIDHTKNT-FDVDRWD	78
Qy	61	KTFVTIERNNGVPSLLNVVTKKGGPILLRPYPDMSFAKYEDCGSVSAFKIADVDFDR	120
Db	79	KTFVTIERNNGVPSLLNVVTKKGGPILLRPYPDMSFAKYEDCGSVSAFKIADVDFDR	138
Qy	121	LWVLDSGLVNNQPMQSPKLLTFDLKTSKLVKQVEIPHNTAVNATTGMGELVSLAVQAID	180
Db	139	LWVLDSGLVNNQPMQSPKLLTFDLKTSKLVKQVEIPHNTAVNATTGMGELVSLAVQAID	198
Qy	181	RTNTWVYIADKRGGLIMYQNSDDSFHRLTSNTFDYDPRYTKLVVAGESFTVKGICGIA	240
Db	199	RTNTWVYIADKRGGLIMYQNSDDSFHRLTSNTFDYDPRYTKLVVAGESFTVKGIGIA	258
Qy	241	LSPTVNNLYSPSSHGLIYYVDTQFRNPQYEEENNQYEGSQDILNTOSFGKVVSKGVL	300
Db	259	LSPTVNNLYSPSSHGLIYYVDTQFRNPQYEEENNQYEGSQDILNTOSFGKVVSKGVL	318
Qy	301	FLGLVGNSGIACVNEHVLQRESFDVVAQNEETLQMIVSMKIMENLPQSGRINDEGNEY	360
Db	319	FLGLVGNSGIACVNEHVLQRESFDVVAQNEETLQMIVSMKIMENLPQSGRINDEGNEY	378
Qy	361	MLALSNRMQKIINDDFNFDVNFRLGANVDDLMRENTCGRYHQNQAGNQADNQANQ	420
Db	379	MLALSNRMQKIINDDFNFDVNFRLGANVDDLMRENTCGRYHQNQAGNQADNQANQ	438
Qy	421	NANNQADNQANQNGNRQNDNRQNDNK	449
Db	439	NANNQADNQANQNGNRQNDNRQNDNK	467

RESULT 2

S39194
royal jelly protein RJP57-2 - honeybee
C;Species: Apis mellifera (honeybee)
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S39194
R;Klaudiny, J.; Hanes, J.; Kullafajova, J.; Albert, S.; Simuth, J.
A;Description: Molecular cloning of two cDNAs from the head of the nurse honey bee (Apis mellifera) submitted to the EMBL Data Library, September 1993
A;Reference number: S39193
A;Accession: S39194
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-464 <KLA>
A;Cross-references: UNIPROT:Q17061; UNIPARC:UPI000012F56A; EMBL:Z26319; NID:9433530; PID:

Query Match 48.2%; Score 1347; DB 2; Length 464;
Best Local Similarity 56.9%; Pred. No. 1.9e-81;
Matches 261; Conservative 84; Mismatches 94; Indels 20; Gaps 8;
QY 3 VNHQKSNANLAHSMKVIYEWKHIDPFGSDERRDAAIKSGEPDHTKNYPFDVDRWRDKT 62
DB 22 VVRENSGKLTNTLVNHKWKYLDYDFDNRQAAIQSGEYRTKNYPFLDVQWQHNKT 81
QY 63 FVTIERNGVPSSLVNVTNKKGGPGLLRYPYDMSFAKYEDCSGIVSAFKIAVDKPDRLW 122
DB 82 FLAVIRYNGVPSSLVNVSVDKTGNGGRLLQPYDMSFAKYEDCSGIVSAHKIAIDEYERLW 141
QY 123 VLDGSLVNNQPMCSPKLLFDLTKSLVKQVEIPHNIAVNAATTGMGELVSLAVQAI 182
DB 142 VLDGSLVNNQPMCSPKLFAFDLNTSOLKQVEIPHDV--ATTGKGLVSLTVQAMDS 198
QY 183 NTMYVIADEKGEGLIMYQNSDDSPHRLTSNTFDYDPRTYKLTIVAGESFTVK--NGTCGI 239
DB 199 NTMYVVDNKT-LIIYQNADDSPHRLSSHTLHNS--DRMSQOENLTIKEDVKNKYGM 255
QY 240 ALSPTNLYNYPSSHLGYVYDTEQFPNPOYEENNVQYEGSQDILNTQSGFKVSKNGV 299
DB 256 ALSPTNLYNYPSSENLYYNTESLMKSGENQGNQYQVDFSDQLTVKAVSKNGV 315
QY 300 LFLGLVNGSIACVNEHQVLORESFDVVAQNEETLQIMVSKIMENLPQSGRNDPQSGNE 359
DB 316 LFLGLANNT-LSCWNEHQSLDRQIDYVARNEDTLQMVSMKKIQNVYQSGRVNNTQSGNE 374
QY 360 YMLALSNRMOKIINDFNFDNFRILGANVDDLMRNTCRGRYHQNAGNQADNQADN 419
DB 375 YLLALSDRNQVNLNDLNLHVNFIQLGANVNDLIRNRCANFDNQDNNHYNH----N 430
QY 420 QNANNQADNQANQKNGRQNDNRQNDKONGNRQNDN 458
DB 431 QARHSSKSDN-----QNNQHNDQARHSSKSN-NRHN 463

RESULT 3

A25696
Yellow protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C;Accession: A25696; A25683
R;Geyer, P.K.; Spana, C.; Corcos, V.G.
A;Title: On the molecular mechanism of gypsy-induced mutations at the yellow locus of Drosophila
EMBO J. 5, 2657-2662, 1986
A;Reference number: A25696; MUID:87053835; PMID:3096713
A;Accession: A25696
A;Molecule type: DNA
A;Residues: 1-541 <GBY>
A;Cross-references: UNIPROT:P09957; UNIPARC:UPI000011F616; GB:X04427; NID:98835; PIDN:CA
A;Note: the authors translated the codon AAC for residue 364 as Asp
R;Chia, W.; Howes, G.; Martin, M.; Meng, Y.B.; Moses, K.; Tsubota, S.
EMBO J. 5, 3597-3605, 1986
A;Title: Molecular analysis of the yellow locus of Drosophila.
A;Reference number: A25683

A;Accession: A25683
A;Molecule type: DNA; mRNA
A;Residues: 1-541 <CHI>
A;Cross-references: UNIPARC:UPI000011F616; GB:X04703
C;Genetics:
A;Gene: FlyBase:Y
A;Cross-references: FlyBase:FBgn0004034
A;Introns: 80/1
Query Match 15.3%; Score 427; DB 2; Length 541;
Best Local Similarity 28.0%; Pred. No. 1.3e-20;
Matches 116; Conservative 85; Mismatches 165; Indels 48; Gaps 13;
QY 14 AHSMKVIYEWKHIDPFGSDERRDAAIKSGEPDHTKNYPFDVDRWRDKTFTVTTIER-NGV 72
DB 22 AYKLOERYSWSQLDFAPPNTRLKQALASGDYIPQNALPVGVEHFGNRLFTVTPRWRDGI 81
QY 73 PSSLVNVT-NKKKGKGPGLLRYPYDMSFAKYEDC-SGIVSAFKIAVDKFDRLWLDSGLV- 129
DB 82 PATLTYYNMDRSITGSPFLIPYDMSRTAGDCANSITTAYRIKVDCEGRLWLDTGTVG 141
QY 130 --NNNQPMCSPKLLTLDLTKSLVKQVEIPHNIAVNAATTGMGELVSLAVQAI 183
DB 142 IGNTTNPCEYAVNVFDLTDTRIRYELP-GVDTNPNTFIANI-----AVDIGKNCD 194
QY 184 TMVYIADEKGEGLIMYQNSDDSPHRLTSNTFDY-DPRYTKLTIVAGESFT-VKNGIGICIAL 241
DB 195 AVAYFADELGYGLIAYSWELNKSWRFSAHSYFPDPLRGDFNVAGINFQWGEERGIFGMSL 254
QY 242 SPVTNN-----LYYSPSSHLGYVYDTEQFPNPOYEENNVQYEGSQDIL-----NTQSF 290
DB 255 SPIRSDGYRTLYESPASHRQFAVSTRILRDETRTDSY-----HDFVALDERGPNSHTT 309
QY 291 GKVSKNGVLFGLVNGSIACVNEHQVLORESFDVVAQNEETLQIMVSKIMENLPQSG 350
DB 310 SRVMSDDGIELFNLIDQNAVGCWHSSWPYSPQPHGIVDRDDVGLVFPADVKKIDE----- 363
QY 351 RINDPGEYMLALSNRMOKIINDFNFDNFRILGANVDDLMRNTCRGRYH 404
DB 364 -----NKNVWVLSDRMPVFLSLDYSNTFNRIYTAPLATLIENTVCDLRN 410

RESULT 4

JC7253
Yellow-B protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: JC7253
R;Maleszka, R.; Kucharski, R.
A;Title: Analysis of Drosophila yellow-B cDNA reveals a new family of proteins related to rans.
A;Reference number: JC7253
A;Accession: JC7253
A;Molecule type: mRNA
A;Residues: 1-453 <MAL>
A;Cross-references: UNIPROT:Q9VJ15; UNIPARC:UPI0000083EA4; GB:AC005119
A;Experimental source: head
A;Comment: This protein, a secreted protein, is involved in neural function, cuticle development.
C;Genetics:
A;Gene: yellow-B
A;Map position: 2 left arm
Query Match 15.0%; Score 418.5; DB 2; Length 453;
Best Local Similarity 27.9%; Pred. No. 3.6e-20;
Matches 122; Conservative 84; Mismatches 194; Indels 37; Gaps 12;

QY 16 SMKVIYEWKHIDPFGSDERRDAAIKSGEPDHTKNYPFDVDRWRDKTFTVTTIER-NGVPS 74
DB 21 NLRVAYEWREMDPKYANPDQWNSAIEGRGFKPANVIPPFGLEVAGHRLFTVTPRWRDGPVA 80
QY 75 SLNVV-TNKKKGKGPGLLRYPYDMSFAKYEDCS-GIVSAFKIAVDKFDRLWLVD---SGLV 129
DB 76 SLNVV-TNKKKGKGPGLLRYPYDMSFAKYEDCS-GIVSAFKIAVDKFDRLWLVD---SGLV 129

Db 81 SLAYLDLNDTSSKGPALKPFPPMQAHNLQEAPELVSPPRVRADRCGLRWLSDRISGVL 140
Qy 130 NNNQPMCSPKLLTFDLKTSKLVQVEIPHNIAVNATTGMEGLVSLAVQALDRTNTWYVIA 189
Db 141 EOTKIYGAQLLVYDLHNDLLRRHVLPAQLKQGSLL----LANLAVEDSDCENTFAYAA 196
Qy 190 DEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTAVAGESFTVKGICGIALS-PVTN-- 246
Db 197 DLGSPGLVYVSWKDEESWRVQHHPFDPDMAGNPSINGIEFQWDDGUYGLALSKPLETGY 256
Qy 247 -NLVYSLSSHGLYVYDTEQFRNPQYBENNVOYE-----GSQDILNTQSFQKVSKN-GV 299
Db 257 ATLPHPLCSTTESVDTSLRNKTLATSPMIYREFKVLGSRG-PNTQAGAEFLDPDTGV 315
Qy 300 LFLGLVNGSIACVNEHQVLRQESFDVVAQNEETLQMIYSKIMENLPOSGRINDPEGNE 359
Db 316 LFVALPNLNEVACWRTATDFSHSQSRHNMNDTLVFPFSIKV-----DDQK 362
Qy 360 YMLALSRMOKIINNDFNDFNFRILGANVDDLNRTRCGRYHONAGNQADNQADN 419
Db 363 RLWVLSNQLPVFIYDELYAGSINFRILTASVKEAIENTAC----EIRTSPLPDVINKLGD 419
Qy 420 QNANNQADNQANKON 436
Db 420 LNTNKLKSNASSILRN 436
RESULT 5
TipC protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17414
R;Stege, J.T.; Laub, M.T.; Loomis, W.F.
A;Description: Interaction of tip genes in early Dictyostelium discoideum development.
A;Reference number: Z18774
A;Accession: T17414
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3848 <STE>
A;Cross-references: UNIPROT:O76737; UNIPARC:UPI0000076F0B; EMBL:AF079445; NID:G3420744;
A;Experimental source: strain AX4
C;Genetics:
A;Gene: tipC
C;Function: 72/3
A;Description: required for tip formation
Query Match 10.0%; Score 278.5; DB 2; Length 3848;
Best Local Similarity 20.7%; Pred. No. 1.3e-09;
Matches 118; Conservative 84; Mismatches 226; Indels 143; Gaps 19;
Qy 68 RNNGVPSSLVNVTNKKGGPGL-----RPYP-----DWSFAKYEDCS--- 105
Db 1737 RNILPLSLKSVNEKROKQEQILPOLIIGSIKPPPIQOSLFQISIDGMFIFVPHSHIP 1796
Qy 106 ---GVSAFKIADVDFDLWLVDGLVNNOPMCSFKLLTFDLKTSKLVQVEIPHNIAV 162
Db 1797 VQDSIMKLKSKFATEAWNRYTIKVYGEAPNDEIIQSGLSLSIKDI--KISIPGDCV 1854
Qy 163 NA-----TTGMEGLVSLAVQALDRTNTWY-----IADEKGEGLIMYQON 201
Db 1855 NSGQGENEYPLFIRSSLDIQTTSRGAMGVETITLDANNIQRNQLVDVTNNENNNNN 1914
Qy 202 SDDSFRHTSNTFDYDPRYTKL-----TVAGESFTVK 233
Db 1915 NNLATSTTTTTTNKQSNIKIIAPFKIVQTTSTLLNSESLSLNNIVVTFSYQDFKLM 1974
Qy 234 NGICGIALSPVTNNLYSPSSHGL--YYVD-----TEQFRNPQYBENNVOYE 279
Db 1975 MKIINSIIESNNQNLIQEKMKRYLKKYRDPNECTSDDELEBQLQLENDYNDNNYSN 2034

Qy 280 GSQDILNTQSFQKVSQKNGVL--FLGLVNGSIACVN-EHQV-----LQRE 322
Db 2035 GNNN--NNNSNQLPVKESQLKYSLSLEKGEFLINDDHKISSPIKLLSIGVDGLKSN 2092
Qy 323 SPDVVAQNEETLQMIYSMK-----IMENLPOSGRINDPEGNEYMALSNRMQ 369
Db 2093 IFSFPQKQIATSLSDANMKAGYFNKNIGIWEPLIENWGFSFTSNNSIEGGMVNFNSKIP 2152
Qy 370 KIINDFNDFNFRILGANVDDLNRTRCGRYHONAGNQADNQADNQANN----- 424
Db 2153 LYINIKFIDTSISTYQIWADE-----YYSQ-----QKDKKKNKSNYDNDDEI 2199
Qy 425 --QVADNQNANKQNRQNDNRQNDKQNRQNDKQNRQNDKQNRQNDKQNRQNDKQNRQNDKQND 482
Db 2200 TVSQVANDLIKPADDDQKNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2259
Qy 483 NKQNGRQNDKQNRQNDNRQNDKQNRQNDKQNRQNDKQNRQNDKQNRQNDKQNRQNDKQNRQND 513
Db 2260 NNN 2289
RESULT 6
S71629
sensory transduction histidine kinase dhkA - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S71629
R;Wang, N.; Shaulsky, G.; Escalante, R.; Loomis, W.F.
EMBO J. 15, 3890-3896, 1996
A;Title: A two-component histidine kinase gene that functions in Dictyostelium developme
A;Reference number: S71629; MUID:96324397; PMID:8670894
A;Accession: S71629
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-2150 <WAN>
A;Cross-references: UNIPROT:Q23863; UNIPARC:UPI0000017B18D; EMBL:U42597
A;Experimental source: strain AX4
C;Genetics:
A;Gene: dhkA
A;Map position: 6
C;Keywords: autophosphorylation; phosphoprotein; phosphotransferase; two-component regul
F;2076/Binding site: phosphate (Asp) (covalent) #status predicted
Query Match 9.5%; Score 267; DB 2; Length 2150;
Best Local Similarity 20.2%; Pred. No. 3.3e-09;
Matches 126; Conservative 64; Mismatches 207; Indels 226; Gaps 21;
Qy 4 NHQRKSANNLAHSMKVIYEWKHIDFEGSDERR-----DAAIKGGEFPHTKNYPPD- 54
Db 235 NNGGNNNNNITDPTKSKRHSYETNIGSHQRRKSIQSLIANSIHS--FSKLKNKPLSS 292
Qy 55 -----VDRWRDKTFVTIER-----NNGVPSL 76
Db 293 STPSTVATCGAVNN 351
Qy 77 NVVTNKKGKGLLPYPYDWSFAKYEDCSGVSAFKIADVDFDLWLVDGLVNN--NQ 134
Db 352 NCGSNGSGNGIPLSP-----RNLSLNSGVNVSPRIHL-----NNLNNSNLP 397
Qy 135 MCSPKLLTFDLKTSKLVQVEIPHNIAVNATTGMEGLVSLAVQALDRTNTWYIADEKGE 194
Db 398 PLSPRHINFINVNLNNN-----NNNINPNNNP----- 427
Qy 195 GLIMYQNSDDSFHRLT--SNTFDYDPRYTKLTAVAGESFTVKGICGIALSPVTNNLYSP 252
Db 428 ----NNSNNNNNVSPRNNNNHISPR-----GSNISPRNNGSGSTT 464
Qy 253 LSSHGLYVYDTEQFRNPQYBENNVOYEGSQDIL-----NTQSGFKVSVKNGVLFLGLVNGS 308
Db 465 ISP-----RNISNNNNIINNINNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 513
Qy 309 GIACVNEHQVLRQESFDVVAQNEETLQMIYSKIMENLPOSGRINDPEGNEYMALSNRM 368

```

Db      514 -----|||:::||::|||::|||-----TLPIVSLTSSNNNQNNTNPS-----537
Qy     369 QKIINDFNFNVFRILGANVDLDMENTRCGRVHNOAGNQADNQADNQ--ANNQN 426
Db      538 ---INN---NGRNGHCIIOTISEILGNKPVYVYNGNNNNNNNTTNSTTSNNITNNN 591
Qy     427 ADQNAV-----KONG-----RQNDN 443
Db      592 NNNNNINNVLTSPRKRTKGHSKTNSIQDFTSSMMGGDDISGAGSGGLRRNKODN 651
Qy     444 ROND---NQKNGFNQDNKNGFNQDNKNGFNQDNKNGFNQDNKNGFNQDNKNGNRQ 500
Db      652 DENDCNSNTTNSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 711
Qy     501 NDNONQNDNRNDNOVHSSKL 523
Db      712 NNNNNNNNNNNNNNNNYHGATM 734

RESULT 7
C71618
hypothetical protein PFB0315w - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C:Accession: C71618
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A>Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: C71618
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1712 <GAR>
A:Cross-references: UNIPROT:O96160; UNIPARC:UIP000007A674; GB:AEO01386; GB:AEO01362; NID
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0315w

Query Match          9.3%; Score 261; DB 2; Length 1712;
Best Local Similarity 21.6%; Pred. No. 5.9e-09;
Matches 138; Conservative 106; Mismatches 207; Indels 188; Gaps 30;

Qy      8 KSANLAHSMKVIEWKHIDFDGSDERRDAAIKSGEFHT---KNYPFDVDRWRDKTF 63
Db     129 KIKNPITSHLKSNTEYNFPVKLSNFSNFKGCSHKDNVINETMDQHKEQLNNNDIKKLLY 188
Qy     64 -VTIERNNGVPSSLNVVNTKKGGKGPILLRPYPDWMSFAKYEDCSGIVSAPKIAVDKFDRLW 122
Db     189 DYCIFREDTIKTNTNISVNK-----PKLTPDLTKSKLVQVEIP-----HN 159
Qy     123 VLD-SGLVNNQPMS-----PKLTPDLTKSKLVQVEIP-----HN 159
Db     221 YMDNNNIKSNSSYCSYSNKNQNNVNHTHLKTEFLNEKNSHTQNEQISPLLDGLQNNHN 280
Qy     160 IAVNATTGMGELSVLAQAIDRTWTMYIADEKGEGLIMYQNSDDSPHRLTSTNTPDYDP 219
Db     281 SATKFHNNI-----YDNNNSLVNYKSDGK-----IDLHNK 310
Qy     220 YTCLKTVAGESPTVKNIGICGIAL----SPVTNNLYYSPSSHGLYYVDT-----EQFRNPQ 270
Db     311 MKKIE-----TDKNGIITLEKKKHDEKYNNIFLNPLDNSNNNVITTCDNKESYRNST 364
Qy     271 YEENNVYE-----GSQDILNTQSFGKVVSRKGVLFGLGVNSGACVNEHQVL-----319
Db     365 SDMIINKIFEKMMNEKKVILKMNCFNDVIKKKITMAKEKILNSN-STINMKKVSFYNSKDE 423
Qy     320 ----ORES---FDVVAQEETLOMIV-SKMIME-NLPQSGRIINDPEGNEYMLALSNMOK 370
Db     424 DLNFEKENSXYGYKRENGQEDINVIKNMKRNNINIDNNNDINIKNDSVSKNIHHNNKK 483
Qy     371 IINDDFNFD-----VNFRIILGANVDDLMENTRCGR-----YHQNAGNQ--ADNQ 415

```

Db 484 KRDDDFPPNNSAGLLDLDFLCRKVKLEILKVNQSSKKCKKILTNHNSSDNQCHSSDNQ 543

Qy 416 N--ADNQ--ANNQN--ADNQANKQNGRQNDNR-----QNDNKQN 451

Db 544 NCHSSDNQCHSSDNQCHSSDNQCDSNACNCKDEKKRKKKKIKKKQKQKSNKSK 603

Qy 452 GNRQ-----NDNKQNGRQNDN--KQNGRQNGKQNDNKQN--GNRQNDNKRNGNRQ 500

Db 604 NKRETQSKISNNNNNNNNQCDNMGDQRINNENMDKQNVNIQNGEGFNKKNNNDLL 663

Qy 501 N-----DNQNNQNDNRNDNQ-VHSSKL 523

Db 664 NVYISPNNINHSLSSTCEKKNKEDNKQNDNKFLNSSKKM 702

RESULT 8

T09080

probable chloroquine resistance protein CG2 (strain HB3) - malaria parasite (Plasmodium C/Species: Plasmodium falciparum

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T09080

R;Su, X.Z.; Kirkman, L.A.; Fujioka, H.; Wellem, T.E.

Cell 91, 593-603, 1997

A>Title: Complex polymorphisms in an 330 kba protein are linked to Chloroquine-resistant A;Reference number: Z16556; MUID:98054002; PMID:9393853

A;Accession: T09080

A>Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2819 <SUX>

A;Cross-references: UNIPROT:O15792; UNIPARC:UPI00000785E5; EMBL:AF030693; NID:g2642515;

A;Experimental source: strain HB3; from Honduras

C/Genetics:

A;Gene: cg2

C;Keywords: toxin resistance

Query Match 9.0%; Score 251; DB 2; Length 2819;

Best Local Similarity 25.1%; Pred. No. 5.5e-08;

Matches 113; Conservative 75; Mismatches 154; Indels 108; Gaps 30;

Qy 141 LTFDLKTSKLKQVLPHPHIANVATTGMGELVSLAVQADRTN--TWVYIADEKGEGL-- 196

Db 1997 LNDRKISNAKRYTFH-----TNMDIFN-----DDNCCINIINVEDNKEENIKD 2043

Qy 197 IMY-----QNSDDSPHRLT-SNTFDYDPRYTKLTVAGESFTV----KNGICGIALSP 243

Db 2044 LYKKLKTNEVEKVDNEFTQVTDNNIIENPKKSTQNEQHNTINENG----- 2095

Qy 244 VTNNLIYSGPLSHGLYYVDTEQFRNPQYBENNVOYSGSDILANTQSGKVVSRKGVLPGLG 303

Db 2096 --NMV-----TYSLINSTLTNNIHMRKWKYLINTYCF-----NNVIMPFQ 2134

Qy 304 LVNGSGI---ACVNEHVQLORSEFVVAQNEETLQWIVSMKIMENLPQSGRINDPEGNEY 360

Db 2135 TTQNKYLLNRRLTKAFLRSLKFDNFNDIKSYKKYKVEINYCDNNHNNKNDTAQQVIH 2194

Qy 361 MLALSNMOKIINNDFNFN-----DVNFRILGANVDD-----IMR 395

Db 2195 YLKEDQKEKELINFDBHIINYSMDNIWVSQIHLYLTHGLSYFENVGEEVDEDAWFYCLQK 2254

Qy 396 NTRCGRYHNQAGN--QNAQDQ-NADNQ--NANNQVADNQ--NANKONG-NRQN-DNRQN 446

Db 2255 KKKINGDDNKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDK 2314

Qy 447 -DNKONG-NRQN-DNKONG-NRQN-DNKONG-NRQNG-NKQNG-NKQNG-NRQN-DNKRN 496

Db 2315 GDNKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDK 2374

Qy 497 GNRQNDNQNNQNDNR--NDNQVHHSSKLH 524

Db 2375 GDNKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDKMGNDK 2404

C;Keywords: surface antigen

```
Query Match      8.6%; Score 239.5; DB 2; Length 518;
Best Local Similarity 20.3%; Pred. No. 2.8e-08;
Matches 99; Conservative 74; Mismatches 137; Indels 177; Gaps 20;

QY 128 LVNNQPMCSFKLLTFDLKTSKLVKQVEIPHNTAVNATTGGMGLVSLVAQAD--RNTNM 185
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 MMSNENKMPDKPVENNLQNNILKR-----DNIIRKPVKLSNLLFGQVDIKLVVDM 130
QY 186 VYIADEKGEGLIMYQNSDDGFFHLRTSNTFDYDPRYTKLTVAGSFTVKNGICGIALSP-- 243
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 TFYNDWN-----LFKOTDGMF-----GLAGKELSCRN-----ISAWPNI 164
QY 244 -VTNNLYYS-----PLSSHGLYYVDTEQFRNPQYEB-----NNV----- 276
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 165 LENNSIFALDINLPNDAIKTYPTFPVNSVGTLYEYDLKKGNDKSKSDQINNVKDNM 224
QY 277 -----QYEGSQDILN-----QMVSMK-----IMENLPQSGRINDPEGNEYMALSNR 367
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 285 VCNNIEFGKSSNWQAIIDLSQQCLVLPKFWLSIMEYLP----- 324
QY 368 MQKIINDDFNFDVNFPRILGANVDDLNRNTRCGRYHQNAGNQADNQADNQANNQNA 427
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 325 ----VNKD-----DD-----RCIR-KMNPNNNNNNKNDNNNNNNKNN 359
QY 428 DNQVANKQNGRQNDNQNGKNGRQNDNQNGKNGRQNDNQNGKNGRQNGKQ----- 480
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 360 DNNN-----NNKNDNNNNNNKNDNNNNNNKNDNNNNNNKNDNNNGDNDVYEENSLP 415
QY 481 -----NDNKQNGRQNDKNGRQNDNQ-----NNQND 509
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 416 RMCSVDHNRNPLPLTKFPLSDNDIVSDNNIYSSPESKNGKNEKQAIYIPDLNLI 475
QY 510 NNRNDNQ 516
D  : : : :
Db 476 NDKKNQ 482

RESULT 13
T14004
trfa protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14004
R;Saito, J.; Adachi, H.; Sutoh, K.
J. Biol. Chem. 273, 24654-24659, 1998
A;Title: Dictyostelium TRFA homologous to yeast Ssn6 is required for normal growth and
A;Reference number: Z17852; MUID:98406112; PMID:9733762
A;Accession: T14004
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1390 <SAI>
A;Cross-references: UNIPROT:O77033; UNIPARC:UPI000007B414; EMBL:AB009080; NID:d1228566;
A;Gene: trfa
A;Introns: 333/3; 364/3; 637/1

Query Match      8.5%; Score 236.5; DB 2; Length 1390;
Best Local Similarity 21.7%; Pred. No. 1.8e-07;
Matches 94; Conservative 42; Mismatches 128; Indels 169; Gaps 17;

QY 239 IALSPVTNNLYYSPLSHGLYYVDTEQF-----RNPQVEENNVOYEGSQDILNTQSF 290
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 481 IRLNPLFLSEVMY-----DLGTLYESCHQHTDSLQAYQAAELDPNKHQISRLATLRAQVS 536
QY 291 GKVSKNG-----DLGTLYESCHQHTDSLQAYQAAELDPNKHQISRLATLRAQVS 309
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 537 GKPIGKDGYLQNGEHGKGKSTPMIIEPNSPQTGAMESLGKGGQNRNNGNNNSFV 596
```

```
QY 310 --IACVNEH-QVLQRESFDVVAQNBTLOMI-----VSMKIM 343
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 597 PELAEINSHLPEDMRNNSLSPSSNELNLSLIDRKTERGERGEDMHNHSHHSQYSNMSMNMM 656
QY 344 ENLPQSGRINDPEGNEYMALSNRMOKIINNDNFENDV-NFRILGANVDDDLMTNRCGRY 402
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 657 NNNNNNNNN-----NMNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNH 708
QY 403 --HNQVAGNQADNQADNQANNQADNQANKQNG----- 437
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 709 NNHQMNYNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 767
QY 438 -NRQN-DNRQN-----DNKO-----NGNRQNDN-----KNGRQND 467
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 768 DNRDNRDNRDNRDNRDNRDNRDNRDNRDNRDNRDNRDNRDNRDNRDNRDNRDNRDNR 827
QY 468 NKQNGRQNGKNDKQNG-----NRQNDKNGRQND 502
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 828 NYNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 887
QY 503 NQNNQNDNRNDN 515
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 888 NNNNNNNNNNSN 900

RESULT 14
T18440
hypoetical protein C0425w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18440
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Accession: T18440
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-4550 <LAW>
A;Cross-references: UNIPROT:O77336; UNIPARC:UPI0000110116; EMBL:Z98547; NID:e1325376; PFI
C;Genetics:
A;Map position: 3
A;Note: C0425w

Query Match      8.1%; Score 227.5; DB 2; Length 4550;
Best Local Similarity 18.5%; Pred. No. 3.8e-06;
Matches 123; Conservative 77; Mismatches 204; Indels 262; Gaps 22;

QY 69 NNGVPSSLNVVT---NKGKGGPLLRP-----YPDWSFAKYEDCSGIVSAFKIA 114
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1529 NNNNINNNNVQEDYKMKGKGGSHKQKHKSTNYNQDDIYDNDFSSI--CSLLSSSLSTN 1586
QY 115 VDKFRLWLVDLGLVNNNQPMCSFKLLT---PDLKTSKLVKQVEIPHNTAVNATTGME 170
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1587 ND-----IDSSYVNNNSLYNSSSMFSDNDDCFSLCYSSVSSSYEYDDINNVNLKNKIHN 1639
QY 171 LVSLAVQAIADRTMTWYIADEKGEGLIMYQNSDDGFFHLRTSNTFDYDPRY-----TKLTV 225
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1640 FPSFYKNELNNNN-----NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1684
QY 226 AGESF--TVKNGICGIALSPVTNNL-----YYSPLSHGLYYVDTEQFRNPQVEEN 274
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1685 SRSFPGWSLYNTSDNISSEISNNLSFSKSNYCSSISDHEI-BKDVITYIRNTVHRII 1743
QY 275 NVQYEG-----SQDILNTQSPGKVVVKNQVFLGLVNGSGIACVNEHQVLR----- 321
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1744 NRWKDQKNTGSKKRDMSNKKGDKSCNKK-----ICDNKKNIYDNKKLIYD 1790
QY 322 -----ESPDVVAQNEETQMTVSMKIME-NLPQSGRINDPEGNEYMAL----- 364
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1791 NKDSSTDAPVENIDHLIEKEEIDNILNGLTYNLEK-----NNNNNNNNNNNNNNNNNN 1845
QY 365 --SNR--MQKIIN-----NDFNFNDVN-----PRILGANVD 391
```


This Page Blank (Page 1)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 18:54:38 ; Search time 242.593 Seconds
(without alignments)
1523.941 Million cell updates/sec

Title: US-10-525-567-3

Perfect score: 2796

Sequence: 1 AAVNHQRKSNANLAHSMKVI.....NNQNDNRNDNQVHHSSKLH 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2773	99.2	544	1 MRJP3 APIME	Q17060 apis mellif
2	1671.5	59.8	468	2 Q5VK55 APICC	Q5vk55 apis cerana
3	1658.5	59.3	463	2 Q6MMJ0 APICE	Q6mmj0 apis cerana
4	1658.5	59.3	463	2 Q50H66 APICE	Q50h66 apis cerana
5	1634.5	58.5	452	1 MRJP2 APIME	Q77061 apis mellif
6	1572.5	56.2	437	2 Q6W3E3 APIME	Q6w3e3 apis mellif
7	1486.5	53.2	443	2 Q6IMJ9 APIME	Q6imj9 apis mellif
8	1437.5	51.4	579	2 Q6QN15 APICE	Q6qn15 apis cerana
9	1427	51.0	598	2 Q5VK56 APICC	Q5vk56 apis cerana
10	1420.5	50.8	432	1 MRJP1 APIME	Q18330 apis mellif
11	1420.5	50.8	432	2 Q548D6 APIME	Q548d6 apis mellif
12	1407	50.3	598	1 MRJP5 APIME	Q97432 apis mellif
13	1403.5	50.2	433	2 Q5VLK2 APICC	Q5vle2 apis cerana
14	1402.5	50.2	433	2 Q6MMJ1 APICE	Q6mmj1 apis cerana
15	1402	50.1	485	2 Q6QN16 APICE	Q6qn16 apis cerana
16	1347	48.2	464	1 MRJP4 APIME	Q17061 apis mellif
17	1218	43.6	416	2 Q6TGR0 APIME	Q6tgr0 apis mellif
18	1132.5	40.5	423	2 Q4ZJX1 APICE	Q4zjx1 apis mellif
19	834	29.8	222	2 Q5I222 APICE	Q5i222 apis cerana
20	819	29.3	220	2 Q5I223 APICE	Q5i223 apis cerana
21	778.5	27.8	222	2 Q5I224 APICE	Q5i224 apis cerana
22	490.5	17.5	186	2 Q6M24 APIDO	Q6m24 apis dorsat
23	463.5	16.6	406	2 Q7Q4T5 ANOAGA	Q7q4t5 anopheles g
24	454.5	16.3	463	2 Q9V4C0 DROME	Q9v4c0 drosophila
25	451	16.1	411	2 Q6DLY9 APIME	Q6dly9 apis mellif
26	444	15.9	461	2 Q7PHB5 ANOAGA	Q7phb5 anopheles g
27	433.5	15.5	432	2 Q9W1R1 DROME	Q9w1r1 drosophila
28	433	15.5	568	1 YELL_DROU	O02437 drosophila
29	431	15.4	568	1 YELL_DROMD	Q9gp71 drosophila
30	429	15.3	541	1 YELL_DROVA	Q9bi17 drosophila
31	428	15.3	568	1 YELL_DROGU	Q9gp81 drosophila

32	427	15.3	541	1 YELL_DROMA	P62408 drosophila
33	427	15.3	541	1 YELL_DROME	P09957 drosophila
34	427	15.3	541	1 YELL_DROSI	P62407 drosophila
35	426	15.2	462	2 Q7PMG1 ANOAGA	Q7pmg1 anopheles g
36	426	15.2	497	2 Q7Z0H1_9DIPT	Q7z0h1 drosophila
37	426	15.2	540	2 Q86CU0_9DIPT	Q86cu0 drosophila
38	425	15.2	541	2 Q8ISG5_DROVI	Q8isg5 drosophila
39	423	15.1	494	2 Q7Z0H2_9DIPT	Q7z0h2 drosophila
40	422.5	15.1	426	2 Q9VFV2 DROME	Q9vfv2 drosophila
41	422.5	15.1	546	2 Q5IBN4_9DIPT	Q5ibn4 drosophila
42	419	15.0	541	1 YELL_DROER	Q9b123 drosophila
43	418.5	15.0	453	1 Q9VJIS_DROME	Q9vjis drosophila
44	417	14.9	560	2 YELL_DROPS	Q9b118 drosophila
45	415.5	14.9	412	2 Q9W1R0_DROME	Q9w1r0 drosophila

ALIGNMENTS

RESULT 1

MRJP3 APIME STANDARD; PRT; 544 AA.

AC Q17060;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Major royal jelly protein 3 precursor (MRJP-3) (Bee-milk protein)
DE (Royal jelly protein RJP57-1).
GN Name=MRJP3;
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apoidea; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Head;
RA Klaudiny J., Hanes J., Kulifajova J., Albert S., Simuth J.;
RT "Molecular cloning of two cDNAs from the head of the nurse honey bee (Apis mellifera L.) for coding related proteins of royal jelly.";
RL J. Apicultural Res. 33:105-111(1994).
RN [2]
RP SEQUENCE REVISION TO THE C-TERMINUS.
RA Albert S., Klaudiny J., Simuth J.;
RT "Newly discovered features of the updated sequence of royal jelly protein RJP571; longer repetitive region on C-terminus and homology to Drosophila melanogaster yellow protein.";
RL J. Apicultural Res. 35:63-68(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 21-36.
RC TISSUE=Head;
RX MEDLINE=99007754; PubMed=9791542; DOI=10.1007/s000180050229;
RA Schmitzova J., Klaudiny J., Albert S., Schroeder W., Schreckengost W., Hanes J., Judova J., Simuth J.;
RT "A family of major royal jelly proteins of the honeybee Apis mellifera L.";
RL Cell. Mol. Life Sci. 54:1020-1030(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE OF 45-59; 70-77;
RX 106-120; 214-224 AND 243-253.
RC TISSUE=Hypopharyngeal gland;
RX MEDLINE=98055707; PubMed=9395329;
RA Ohashi K., Natori S., Kubo T.;
RT "Change in the mode of gene expression of the hypopharyngeal gland cells with an age-dependent role change of the worker honeybee Apis mellifera L.";
RL Eur. J. Biochem. 249:797-802(1997).
CC -!- FUNCTION: May play an important role in honeybee nutrition. It is found in the royal jelly which is the food of the queen honey bee larva. The royal jelly determines the development of the young honeybee queen.
CC -!- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Hypopharyngeal glands of nurse honey bees.
CC -1- DEVELOPMENTAL STAGE: Produced by the cephalic glandular system of
CC the nurse honey bee.
CC -1- SIMILARITY: Belongs to the major royal jelly protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z26318; CAA81227.1; -; mRNA.
DR Ensembl; ENSAPMG00000007331; Apis mellifera.
DR InterPro; IPR003534; Royaljelly.
DR PANTHER; PTHR10009; Royaljelly; 1.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW Direct protein sequencing; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 20
FT CHAIN 21 544 Major royal jelly protein 3.
FT REPEAT 424 428 1.
FT REPEAT 429 433 2.
FT REPEAT 434 438 3.
FT REPEAT 439 443 4.
FT REPEAT 444 448 5.
FT REPEAT 449 453 6.
FT REPEAT 454 458 7.
FT REPEAT 459 463 8.
FT REPEAT 464 468 9.
FT REPEAT 469 473 10.
FT REPEAT 474 478 11.
FT REPEAT 479 483 12.
FT REPEAT 484 488 13.
FT REPEAT 489 493 14.
FT REPEAT 494 498 15.
FT REPEAT 499 503 16.
FT REPEAT 504 508 17.
FT REPEAT 509 513 18.
FT REPEAT 514 518 19.
FT REPEAT 519 523 20.
FT REGION 424 523
FT CARBOHYD 183 183
FT SEQUENCE 544 AA; 61662 MW; 4C8FFFC8A2759F52 CRC64;
Query Match 99.2%; Score 2773; DB 1; Length 544;
Best Local Similarity 99.4%; Pred. No. 4.1e-167;
Matches 521; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 AAVNHQKSAANLAHSMKVIYEWKHIDPFGSDERRDAAIKSGEFDHTKYPFDVDRWRD 60
Db 21 AAVNHQKSAANLAHSMKVIYEWKHIDPFGSDERRDAAIKSGEFDHTKYPFDVDRWRD 80
Qy 61 KTFVTIERNNGVSSLVNVTNKKGGPILRPYPDWSFAKVEDCSGIVSAFKIADVDFDR 120
Db 81 KTFVTIERNNGVSSLVNVTNKKGGPILRPYPDWSFAKVEDCSGIVSAFKIADVDFDR 140
Qy 121 LWLWDSGLVNNQPMCSFKLLTFDLKTSKLVKQVEIPHNIAVNATTGMGELVSLAVQAD 180
Db 141 LWLWDSGLVNNQPMCSFKLLTFDLKTSKLVKQVEIPHNIAVNATTGMGELVSLAVQAD 200
Qy 181 RTNTMVIYADKEGGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTVAGESFTVKNIGIGIA 240
Db 201 RTNTMVIYADKEGGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTVAGESFTVKNIGIGIA 260
Qy 241 LSPVTNNLYYSPSSHGLIYVDTEQFRNPQYEEENNVOYEGSQDILNTQSGKVVSKNGVL 300
Db 261 LSPVTNNLYYSPSSHGLIYVDTEQFRNPQYEEENNVOYEGSQDILNTQSGKVVSKNGVL 320
Qy 301 FLGLVGNGLIACVNEHQVLORESFDVVAQNEETLQIMVSKIMENLPQSGRINDPEGNEY 360
Db 321 FLGLVGNGLIACVNEHQVLORESFDVVAQNEETLQIMVSKIMENLPQSGRINDPEGNEY 380

Qy 361 MLALSNRMQKIINNDNFNFNDVNFRIILGANVDDILMRNTRCGRYHONAGNQADNQADNQ 420
Db 381 MLALSNRMQKIINNDNFNFNDVNFRIILGANVDDILMRNTRCGRYHONAGNQADNQADNQ 440
Qy 421 NANNQADNQANQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 480
Db 441 NANNQADNQANQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 500
Qy 481 NDNKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 524
Db 501 NDNKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 544
RESULT 2
QSVK55 APICC
ID QSVK55 APICC PRELIMINARY; PRT; 468 AA.
AC QSVK55;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Major royal jelly protein MRJP2.
OS Apis cerana cerana (Oriental honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=94128;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Su S., Chen S., Albert S.;
RL "Molecular cloning of MRJP2 cDNA from Apis cerana cerana in China.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY392758; AAR83083.1; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
SQ SEQUENCE 468 AA; 53060 MW; 5B2A6ARF4C530C84 CRC64;

Query Match 59.8%; Score 1671.5; DB 2; Length 468;
Best Local Similarity 66.4%; Pred. No. 1.6e-97;
Matches 308; Conservative 74; Mismatches 65; Indels 17; Gaps 3;
Qy 6 QRKSANLAHSMKVIYEWKHIDPFGSDERRDAAIKSGEFDHTKYPFDVDRWRD 65
Db 21 QRKSANLAHSMKVIYEWKHIDPFGSDERRDAAIKSGEFDHTKYPFDVDRWRD 80
Qy 66 IERNNGVPSLVNVTNKKGGPILRPYPDWSFAKVEDCSGIVSAFKIADVDFDR 125
Db 81 ILKYDGVPTSLNISMNKIKGGGLLPYPDWSFAKVEDCSGIVSAFKIADVDFDR 140
Qy 126 SGLVNNQPMCSFKLLTFDLKTSKLVKQVEIPHNIAVNATTGMGELVSLAVQAD 185
Db 141 SGLINRTEPICAPKLHVFDLKNKTLKQIEIPHDIANVATTGKGLVSLVQAD 200
Qy 186 VYLADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTVAGESFTVKNIGI 245
Db 201 VYLADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTVAGESFTVKNIGI 260
Qy 246 NNLYYSPSSHGLIYVDTEQFRNPQYEEENNVOYEGSQDILNTQSGKVVSKNGVL 304
Db 261 NNLYYSPSSHGLIYVDTEQFRNPQYEEENNVOYEGSQDILNTQSGKVVSKNGVL 320
Qy 305 VGNISGLIACVNEHQVLORESFDVVAQNEETLQIMVSKIMENLPQSGRIND 364
Db 321 VGNISGLIACVNEHQVLORESFDVVAQNEETLQIMVSKIMENLPQSGRIND 380
Qy 365 SNRMQKIINNDNFNFNDVNFRIILGANVDDILMRNTRCGRYHONAGNQADNQADNQ 424
Db 381 SNRMQKIINNDNFNFNDVNFRIILGANVDDILMRNTRCGRYHONAGNQADNQADNQ 428
Qy 425 QNADNQANQKQNGRQNDNQKQNGRQNDNQKQNGRQNDNQKQNGRQNGKQ 468
Db 429 QKNNQN----NNQKNNQKNNQKNNQKNNQKNNQKNNQKNNQKNNQKNNQ 468

13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Major royal jelly protein 2.
GN Name=mrjpl;
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Imjongjirak C., Klinbunga S., Sittipraneed S.;
RT "Cloning, Expression and Genomic Organization of Genes Encoding Major
RT Royal Jelly Protein 1 and 2 of the Honeybee (Apis cerana).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY515689; AAS8857.1; -; Genomic DNA.
SQ SEQUENCE 463 AA; 52462 MW; 930C91C8CC595935 CRC64;

Query Match 59.3%; Score 1658.5; DB 2; Length 463;
Best Local Similarity 69.1%; Pred. No. 1e-96;
Matches 307; Conservative 62; Mismatches 72; Indels 3; Gaps 2;

Qy 6 QRSANNLAHSMKVIYEWKHIDFGSDERRDAAIKSGEDHTKNYPFDVDRMRDKTFVT 65
Db 21 RNSAKNLENSLVNIHEWKIYIDFGSEERRQAAIQSGEYDHTKNYPFDVQWHDKTFTV 80
Qy 66 IERNNGVPSSLNVNKKGGGPLLRLPYDPWSFAKYEDCSGIVSAFKIADVDFDLRLWLD 125
Db 81 ILKYDGVPSLTLMISNKGKGRLLQYPYDWSAENKDCSGIVSAFKIADKDFDLRLWLD 140
Qy 126 SGLVNNQPMCSKLLTDFDLKTSKLVKQVEIPHNIAVNATTGMLGSLVLAQVADRTNTM 185
Db 141 SGLINRTEPICAPKLHVFDLKNTHLQKQIEIPHDIAVNATTGKGLVSLVQVQMDPNTL 200
Qy 186 VYIADKGEGLIMYQNSDDSFHRLTSNTFDYDPRYKLTIVAGESFTVKNGICGIALSPVT 245
Db 201 VYIADHKGDALIVYQNSDDSFHRLTSNTFDYDPRYKLTIVAGESFTVKNGICGIALSPVT 260
Qy 246 NLYYSPSLSHGLYVYDTEQFRNPQY-EENNVOYEGSDIINTQSFQKVSQNGVLFGL 304
Db 261 NLYYSPSLSHGLYVYDTEQFRNPQY-EENNVOYEGSDIINTQSFQKVSQNGVLFGL 320
Qy 305 VNSGIACVNEHQVLORESFDVVAQNEETLOMIVSMKIMENLPOSGRINDPEGNEYMLAL 364
Db 321 VNSGALGCLNEHQVLORESFDVVAQNEETLOMIVSMKIMENLPOSGRINDPEGNEYMLAL 380
Qy 365 SNRMQKIINNDNFNDVNFRLGAVNVDLMRNTCRGYHQNAGNQADNQADNQANN 424
Db 381 SNRMQKIINNDNFNDVNFRLGAVNVDLMRNTCRGYHQNAGNQADNQADNQANN 438
Qy 425 QNADNQANKQNGRQNDNRQNDN 448
Db 439 QKNNNQKNNQKNNQKNNQNTN 462

RESULT 5
MRJP2 APIME
ID MRJP2 APIME STANDARD; PRT; 452 AA.
AC 077061;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Major royal jelly protein 2 precursor (MRJP-2) (Bee-milk protein).
GN Name=MRJP2;
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 18-30.
RC TISSUE=Head;
RX MEDLINE=99007754; PubMed=9791542; DOI=10.1007/s000180050229;
RA Schmitzova J., Klaudiny J., Albert S., Schroeder W., Schreckengost W.,

QBMWJO APICE PRELIMINARY; PRT; 463 AA.
AC QBMWJO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Major royal jelly protein MRJP2 precursor.
GN Name=MRJP2;
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sittipraneed S., Imjongjirak C.;
RT "Molecular Cloning of Major Royal Jelly Protein (MRJP2) cDNA from Apis
RT cerana in Thailand.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF525777; AAM88282.2; -; mRNA.
DR InterPro: IPR003534; Royaljelly.
DR Pfam: PF03022; MRJP; 1.
DR PRINTS: PR01366; ROYALJELLY.
DR Signal.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 463 AA; 52490 MW; 29D92E3749B15992 CRC64;

Query Match 59.3%; Score 1658.5; DB 2; Length 463;
Best Local Similarity 69.1%; Pred. No. 1e-96;
Matches 307; Conservative 62; Mismatches 72; Indels 3; Gaps 2;

Qy 6 QRSANNLAHSMKVIYEWKHIDFGSDERRDAAIKSGEDHTKNYPFDVDRMRDKTFVT 65
Db 21 RNSAKNLENSLVNIHEWKIYIDFGSEERRQAAIQSGEYDHTKNYPFDVQWHDKTFTV 80
Qy 66 IERNNGVPSSLNVNKKGGGPLLRLPYDPWSFAKYEDCSGIVSAFKIADVDFDLRLWLD 125
Db 81 ILKYDGVPSLTLMISNKGKGRLLQYPYDWSAENKDCSGIVSAFKIADKDFDLRLWLD 140
Qy 126 SGLVNNQPMCSKLLTDFDLKTSKLVKQVEIPHNIAVNATTGMLGSLVLAQVADRTNTM 185
Db 141 SGLINRTEPICAPKLHVFDLKNTHLQKQIEIPHDIAVNATTGKGLVSLVQVQMDPNTL 200
Qy 186 VYIADKGEGLIMYQNSDDSFHRLTSNTFDYDPRYKLTIVAGESFTVKNGICGIALSPVT 245
Db 201 VYIADHKGDALIVYQNSDDSFHRLTSNTFDYDPRYKLTIVAGESFTVKNGICGIALSPVT 260
Qy 246 NLYYSPSLSHGLYVYDTEQFRNPQY-EENNVOYEGSDIINTQSFQKVSQNGVLFGL 304
Db 261 NLYYSPSLSHGLYVYDTEQFRNPQY-EENNVOYEGSDIINTQSFQKVSQNGVLFGL 320
Qy 305 VNSGIACVNEHQVLORESFDVVAQNEETLOMIVSMKIMENLPOSGRINDPEGNEYMLAL 364
Db 321 VNSGALGCLNEHQVLORESFDVVAQNEETLOMIVSMKIMENLPOSGRINDPEGNEYMLAL 380
Qy 365 SNRMQKIINNDNFNDVNFRLGAVNVDLMRNTCRGYHQNAGNQADNQADNQANN 424
Db 381 SNRMQKIINNDNFNDVNFRLGAVNVDLMRNTCRGYHQNAGNQADNQADNQANN 438
Qy 425 QNADNQANKQNGRQNDNRQNDN 448
Db 439 QKNNNQKNNQKNNQKNNQNTN 462

RESULT 4
Q50H66 APICE PRELIMINARY; PRT; 463 AA.
AC Q50H66;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

```
RA Hanes J., Judova J., Simuth J.;
RT "A family of major royal jelly proteins of the honeybee Apis mellifera
RL L.";
RL Cell. Mol. Life Sci. 54:1020-1030(1998).
CC -|- FUNCTION: May play an important role in honeybee nutrition. It is
CC found in the royal jelly which is the food of the queen honey bee
CC larva. The royal jelly determines the development of the young
CC larvae and is responsible for the high reproductive ability of the
CC honeybee queen.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Found in the hypopharyngeal glands.
CC -|- DEVELOPMENTAL STAGE: Produced in the cephalic glands of the nurse
CC honeybee.
CC -|- SIMILARITY: Belongs to the major royal jelly protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF000632; AAC61894.1; -; mRNA.
DR Ensembl; ENSAPMG0000004182; Apis mellifera.
DR InterPro; IPR003534; Royaljelly.
DR PANTHER; PTHR10009; Royaljelly; 1.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
DR Direct protein sequencing; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 452 Major royal jelly protein 2.
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
FT SEQUENCE 452 AA; 51074 MW; 25E5B621288FE189 CRC64;
SQ
Query Match 58.58; Score 1634.5; DB 1; Length 452;
Best Local Similarity 68.88; Pred. No. 3.3e-95;
Matches 305; Conservative 55; Mismatches 72; Indels 11; Gaps 1;
QY 6 QRSANNLAHSMKVIYEWKHIDFDGSDERRDAAIKSGEFDHTKYNYPFDVDRWRDKTFVT 65
DB 21 RENSPRNLEKSLNVHIEWKFDYDFGSEERRQAAIQSGEYDHTKYNYPFDVDRWRDKTFVT 80
QY 66 IERNNGVPSSLNVNTKKGKGLLPYPDPWSFAKVEDCGSIVSAFKIAVDKFDRLWVLD 125
DB 81 ILRYDGVPSPLNVISGRTGKGRLLKPYDPWSFAEFKDCSKIVSAFKIAIDKFDRLWVLD 140
QY 126 SGLVNNQPMCSPKLLTFDLKTSKLVQVEIPHNIAVNATTGMSGLVSLAVQAIDRNTM 185
DB 141 SGLVNRTPVCAPKLHVFDLKTSHLQKQIEIPHNIAVNATTGKGLVSLAVQAIDLANTL 200
QY 186 VYIADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTAVAGESFTVKGICGIALSPVT 245
DB 201 VYMAHKGDALIVYQNADDSFHRLTSNTFDYDPRYAKWTIDGESFTLKNGICGIALSPVT 260
QY 246 NNLYSPLSHGLYVYDTEQFRNPQVEENNVOYEGSDIILNTQSFQKVVSKNGVLFGLV 305
DB 261 NNLYSPLSHGLYVYNTAPFMKSFQGENNVQYQGSSEIILNTQSLAKAVSKNGVLFGLV 320
QY 306 GNSGIACVNEHVOVLORESFDVVAQNETLQMIIVSMKIMENLQSGRINDPEGNEYMLALS 365
DB 321 GNSAVGCWNEHQSLOQNLEWVAQNDRTLQMIAGMKIKBELPHVGSNKVPKVEYMLVLS 380
QY 366 NRMQKIINDDNFNDVFRILGANVDDLMENTRCGRYHNNQAGNADNQADNQANNQ 425
DB 381 NRMQKIINDDNFNDVFRILGANVDELIRNTHCVN-----NNQNDNIQNTNNQ 429
QY 426 NADQNAKNGRQNDNRQNDN 448
DB 430 NDNNQNNKNNKNNQNNQNDN 452
RESULT 6
Q6W3E3_APIME
```

```
ID Q6W3E3_APIME PRELIMINARY; PRT; 437 AA.
AC Q6W3E3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Major royal jelly protein MRJP6.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15037093; DOI=10.1016/j.jinsphys.2003.09.008;
RA Albert S., Klaudiny J.;
RT "The MRJP/YELLOW protein family of Apis mellifera: identification of
RT new members in the EST library.";
RL J. Insect Physiol. 50:51-59(2004).
DR EMBL; AY313893; AAQ82184.1; -; mRNA.
DR Ensembl; ENSAPMG0000007331; Apis mellifera.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
DR SEQUENCE 437 AA; 49786 MW; 1B654BB7A7F0B56D CRC64;
Query Match 56.28; Score 1572.5; DB 2; Length 437;
Best Local Similarity 72.28; Pred. No. 2.7e-91;
Matches 294; Conservative 56; Mismatches 56; Indels 1; Gaps 1;
QY 5 HQRSANNLAHSMKVIYEWKHIDFDGSDERRDAAIKSGEFDHTKYNYPFDVDRWRDKTFV 64
DB 23 HQRSKKNLEHSMNVHIEWKIDYDFGSDERKQAAIQSGEYDHTKYNYPFDVDRWRDKTFV 82
QY 65 TIERNNGVPSSLNVNTKKGKGLLPYPDPWSFAKVEDCGSIVSAFKIAVDKFDRLWVLD 124
DB 83 AVIRYDGVPSPLNVISEKINGGCLLPYPDPWSWANYKCCSGIVSAFKIAIDKFDRLWVLD 142
QY 125 DSGLVNNQPMCSPKLLTFDLKTSKLVQVEIPHNIAVNATTGMSGLVSLAVQAIDRNTM 184
DB 143 DSGLVNNQPMCSPKLLTFDLKTSKLVQVEIPHNIAVNATTGMSGLVSLAVQAIDRNTM 202
QY 185 MYVIADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTAVAGESFTVKGICGIALSPV 244
DB 203 TVYIADRGDALIIYQNSDDSFHRLTSNTFDYDPRYTKLTAVAGESFTVKGICGIALSPV 262
QY 245 TNNLYSPLSHGLYVYDTEQFRNPQVEENNVOYEGSDIILNTQSFQKVVSKNGVLFGL 304
DB 263 TNNLYSPLSHGLYVYNNMEPFMKSQVEENNIEYEGIDIFNTQSSAKVSKNGVLFGL 322
QY 305 VNGSGIACVNEHVOVLORESFDVVAQNETLQMIIVSMKIMENLQSGRINDPEGNEYMLAL 364
DB 323 VNSAIGCWNEHQPLQONMDVMAQNEKTLQMIISVKIIQNLAYSGRMNRHKNEMYMLAL 382
QY 365 SNRMQKIINDDNFNDVFRILGANVDDLMENTRCGRYHNNQAGN 411
DB 383 SNRMQKIVNDDNFNDVFRILGANVNNLIKTRCAKSNQNN-NQNN 428
RESULT 7
Q6IMJ9_APIME PRELIMINARY; PRT; 443 AA.
AC Q6IMJ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Major royal jelly protein 7.
GN Name=MRJP7;
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
```

```
RP NUCLEOTIDE SEQUENCE
RX PubMed=15037093; DOI=10.1016/j.jinsphys.2003.09.008;
RA Albert S., Klaudiny J.;
RT "The MRJF/YELLOW protein family of Apis mellifera: identification of
RL new members in the EST library.";
RL J. Insect Physiol. 50:51-59(2004).
CC -I- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK001420; DAA01512.1; -; mRNA.
DR Ensembl; ENSAPMG00000007331; Apis mellifera.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
SQ SEQUENCE 443 AA; 50541 MW; 8916272BA44DB421 CRC64;

Query Match 53.2%; Score 1486.5; DB 2; Length 443;
Best Local Similarity 66.9%; Pred. No. 7.4e-86;
Matches 281; Conservative 53; Mismatches 73; Indels 13; Gaps 3;

Qy 6 QKSAANLAHSMKVIYEWKHIDFGSDERRDAIKSGEDHTKNYPFDVDRWEDKTFVT 65
Db 21 RENSARNLKNLSKVMHEWKYIDYDFGSEKKQAAIQSDEYDHTKNYPFDVDRWEDKTFVT 80
Qy 66 IERNNGVPSSLNVVTKKGGPGLLRYPDWSFAKYEDCSGIVSAFAKIAVDKFDRLWVLD 125
Db 81 VLRYDGVPSLLNVISEKTNGRLLQYPDWSWTKYKDCSGIVSAISAIKDFDLWVLD 140
Qy 126 SGLVNNQPMCSKPLTFDLKTSKLVQVEIPHNIANNATTGMGELVSLVAQAIDRNTM 185
Db 141 SGLVNNQPMCFKPLLVFDLNSQLIKQVDIPHEIAVNTTTEQGRKLSLAQAISVNTL 200
Qy 186 VYIADEKGEGLIMYQNSDDSFHRLTSNTFYDPRYTKLTVAGESFTVKNGICGIALSPVT 245
Db 201 VYIADNKGDLIVYQNSDDSFHRLTSNTFYDPRYTKLTVAGESFTVKNGICGIALSPVT 260
Qy 246 NNLYSPSSHLGYVYDTEQFRNPQYBENNVOYEGSQDILNTQSGFKVSKNGVFLGLV 305
Db 261 NNLYSPSSHLGYVYDTEQFRNPQYBENNVOYEGSQDILNTQSGFKVSKNGVFLGLV 320
Qy 306 GNSGIACVNEHQVLORESFDVVAQNEETLQIMVSKMIMENLPQ-----SGRIINDPGE 359
Db 321 NNTAVGCWNEHQVLORESFDVVAQNEETLQIMVSKMIMENLPQ-----E 376
Qy 360 YMLALSNEHQVLORESFDVVAQNEETLQIMVSKMIMENLPQ-----SGRIINDPGE 419
Db 377 YMLVLTNRMQILNLDLNFNDINFRILGVSDELLENTRC---TNFNTQNDSDSDENNDSD 433

RESULT 8
Q6QN15 APICE PRELIMINARY; PRT; 579 AA.
AC Q6QN15;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Major royal jelly protein MRJPs precursor.
GN Name=MRJP5;
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypopharyngeal gland;
RA Sittipraneed S., Cenphakdee K.;
RT "Molecular Cloning of Major Royal Jelly Protein (MRJPs) cDNA from Apis
RL cerana in Thailand.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY532369; AAS21320.1; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 2.
DR PRINTS; PR01366; ROYALJELLY.
```

```
KW Signal.
FT SIGNAL 1 20 Potential.
SQ SEQUENCE 579 AA; 68289 MW; 8218A56E120244F2 CRC64;

Query Match 51.4%; Score 1437.5; DB 2; Length 579;
Best Local Similarity 49.8%; Pred. No. 1.3e-82;
Matches 280; Conservative 63; Mismatches 64; Indels 155; Gaps 3;

Qy 6 QKSAANLAHSMKVIYEWKHIDFGSDERRDAIKSGEDHTKNYPFDVDRWEDKTFVT 65
Db 24 RENSARNLKNLSKVMHEWKYIDYDFGSEKKQAAIQSDEYDHTKNYPFDVDRWEDKTFVT 83
Qy 66 IERNNGVPSSLNVVTKKGGPGLLRYPDWSFAKYEDCSGIVSAFAKIAVDKFDRLWVLD 125
Db 84 VLRYDGVPSLLNVISEKTNGRLLQYPDWSWTKYKDCSGIVSAISAIKDFDLWVLD 143
Qy 126 SGLVNNQPMCSKPLTFDLKTSKLVQVEIPHNIANNATTGMGELVSLVAQAIDRNTM 185
Db 144 SGIINNTQPMCSKPLHVFDLNTSQIKQVMMPHDIAINATTGGLENLVVQAMDPMNTL 203
Qy 186 VYIADEKGEGLIMYQNSDDSFHRLTSNTFYDPRYTKLTVAGESFTVKNGICGIALSPVT 245
Db 204 VYIADNKGDLIVYQNSDDSFHRLTSNTFYDPRYTKLTVAGESFTVKNGICGIALSPVT 263
Qy 246 NNLYSPSSHLGYVYDTEQFRNPQYBENNVOYEGSQDILNTQSGFKVSKNGVFLGLV 305
Db 264 NNLYSPSSHLGYVYDTEQFRNPQYBENNVOYEGSQDILNTQSGFKVSKNGVFLGLV 323
Qy 306 GNSGIACVNEHQVLORESFDVVAQNEETLQIMVSKMIMENLPQSGRIIN- 353
Db 324 NNSAIGCWNEHQVLORESFDVVAQNEETLQIMVSKMIMENLPQSGRIIN- 382
Qy 354 ----- 353
Db 383 RMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMD 442
Qy 354 ----- 353
Db 443 KMKMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMD 502
Qy 354 -----DPEGNEYMLALSNRMQKILNNDPNFNDYFRILGANVDLMDRNT 397
Db 503 MHRMGRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMD 562
Qy 398 RCGRYHQNAGNQADNQADN 419
Db 563 RCANSNQ-----DNQKH 578

RESULT 9
Q5VK56 APICC PRELIMINARY; PRT; 598 AA.
AC Q5VK56;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Major royal jelly protein MRJPs.
OS Apis cerana (Oriental honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=94128;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Su S., Chen S., Albert S., Zhong B.;
RT "Molecular cloning of MRJPs cDNA from Apis cerana.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY392757; AAR83082.1; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 2.
DR PRINTS; PR01366; ROYALJELLY.
SQ SEQUENCE 598 AA; 70522 MW; DD931CA92F433DF2 CRC64;
```

```
Query Match      51.08; Score 1427; DB 2; Length 598;
Best Local Similarity 48.08; Pred. No. 6.4e-82;
Matches 279; Conservative 64; Mismatches 64; Indels 174; Gaps 3;

QY 6 QRKSANNLAHSMKVIYEWKHIDFDGSDERRDAIAKSGFDHTKNYPDPVDRWRDKTFVT 65
DB 24 RENSRLANSMNVHBEWKLDYDFGSDERQRAAIQSGEYDHTKNYPDPVDRWHDMTFVT 83
QY 66 IERNNGVPSSLVNVTNKKGGPPLLRPYPDMSFAKIVSFAKIAVDKFDRLWVLD 125
DB 84 VLRYKGVPSLVNISKKGNGPPLLQYPDMSWANYKDCSGIYSAYKIAIDKFDRLWVLD 143
QY 126 SGLVNNQPMCPKLLTFDLKTSKLKVKQVEIPHNIANVATTGMLVSLAVQALDRNTM 185
DB 144 SGIINTPMCPKHLVDFLNTSQIKQVMVPHDIAINATTGKGLLENLVVQAMDPMNTL 203
QY 186 VYIADEKGEGLIMVQNSDDSFHRLTSTNTFDYDRTYKLTIVAGESFTVKGICGIALSPVT 245
DB 204 VYIADNKGDLIVYQNSDDSFHRLTSTNTFDYDRTYKLTIVAGESFTVKGICGIALSPVT 263
QY 246 NNLVYSPSSHGLYVDTEQFRNPQYBENNVOYEGSDILNTQSGKVKVSKNGVLFGLV 305
DB 264 NNLVYSPASSLSLYYINTKPKMSQYGTNNVQHEGVQDIENFTQSIKIMSKNGVLPGLM 323
QY 306 GNSGIACVNEHVLQRESFDVVAQNEETLQIMVSMKIMENLPQSGRIN----- 353
DB 324 NNSAIGCVNEHVLQRESFDVVAQNEETLQIMVSMKIMENLPQSGRIN----- 382
QY 354 ----- 353
DB 383 RMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMD 442
QY 354 ----- 353
DB 443 RTNKMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMD 502
QY 354 -----DEGNEYMLALSNRKQKILINDNF 378
DB 503 TMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMD 562
QY 379 NDVNFRLIGANVDDMLNTRCRGRVHQNAGNQADNQNADN 419
DB 563 NEVNFRLIGANVDDMLNTRCRGRVHQNAGNQADNQNADN-----DNQNKIN 597

RESULT 10
MRJPI API ME
ID MRJPI API ME STANDARD; PRT; 432 AA.
AC O18330;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Major royal jelly protein 1 precursor (MRJP-1) (Bee-milk protein).
GN Name=MRJPI.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 39-48; 63-71 AND 361-380.
RC TISSUE=Hypopharyngeal gland;
RA MEDLINE=98055707; PubMed=9395329;
RX Ohashi K., Natori S., Kubo T.;
RT "Change in the mode of gene expression of the hypopharyngeal gland
RT cells with an age-dependent role change of the worker honeybee Apis
RT mellifera L.";
RL Eur. J. Biochem. 249:797-802 (1997).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 20-30.
RC TISSUE=Head;
RA MEDLINE=99007754; PubMed=9791542; DOI=10.1007/s000180050229;
RX Schmitzova J., Klaudivy J., Albert S., Schroeder W., Schreckengost W.,
RA
```

```
RA Hanes J., Judova J., Simuth J.;
RT "A family of major royal jelly proteins of the honeybee Apis mellifera
RL L.";
CC -I- FUNCTION: May play an important role in honeybee nutrition. Most
CC abundant protein found in the royal jelly which is the food of the
CC queen honey bee larva. The royal jelly determines the development
CC of the young larvae and is responsible for the high reproductive
CC ability of the honeybee queen.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Found in the hypopharyngeal glands of the
CC worker honeybee.
CC -I- DEVELOPMENTAL STAGE: Produced in the cephalic glands of both the
CC nurse bee and the forager bee. This bee milk protein changes to
CC alpha-glucosidase in accordance with the age-dependent role change
CC of the worker bee.
CC -I- SIMILARITY: Belongs to the major royal jelly protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; D79207; BAA23639.1; -; mRNA.
DR EMBL; AF000833; AAC61895.1; -; mRNA.
DR Ensembl; ENSAPG00000007331; Apis mellifera.
DR InterPro; IPR009007; Pept Aspartic_cat.
DR InterPro; IPR003534; Royaljelly.
DR PANTHER; PTHR10009; Royaljelly; 1.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR0166; ROYALJELLY.
DR Direct protein sequencing; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 432 Major royal jelly protein 1.
FT CARBOHYD 28 28 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 144 144 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 177 177 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 432 AA; 48886 MW; 9F42BF08D34A1A7B CRC64;

Query Match      50.8%; Score 1420.5; DB 1; Length 432;
Best Local Similarity 65.3%; Pred. No. 1.1e-81;
Matches 265; Conservative 63; Mismatches 65; Indels 13; Gaps 2;

QY 12 NLAHSMKVIYEWKHIDFDGSDERRDAIAKSGFDHTKNYPDPVDRWRDKTFVTIERNNG 71
DB 26 SLNKSPLILHEWKFFDYDFGSDERRQDAILSGEYDKNYPDSIDQWHDKIFVTMLRYNG 85
QY 72 VPSSLVNVTNKKGGPPLLRPYPDMSFAKIVSFAKIAVDKFDRLWVLDGLVNN 131
DB 86 VPSSLVNISKKGNGPPLLQYPDMSFAKYDDCSGIVSASKLAIDKCDRLWVLDGLVNN 145
QY 132 NQPMCSFKLLTFDLKTSKLKVKQVEIPHNIANVATTGMLVSLAVQALDRNTM 188
DB 146 TQPMCSFKLLTFDLTTSQLLKQVEIPHVAVNATTGKRLLSSLAQSLDCNTSDTMVYI 205
QY 189 ADSKGBGLIMVQNSDDSFHRLTSTNTFDYDRTYKLTIVAGESFTVKGICGIALSPVTNNL 248
DB 206 ADEKGBGLIVYHNSDDSFHRLTSTNTFDYDRTYKLTIVAGESFTVKGICGIALSPVTNNL 265
QY 249 YVPSLSHGLYVDTEQFRNPQYBENNVOYEGSDILNTQSGKVKVSKNGVLFGLVNGS 308
DB 266 YVPSVASTSLYYNTQFRSTYDQQNDIHVEGQNILDTQSSAKVSKVSGVLFGLVNGS 325
QY 309 GIACVNEHVLQRESFDVVAQNEETLQIMVSMKIMENLPQSGRINDEGNEYMLALSNRM 368
DB 326 ALGCWNEHRLTERRNIRTVAQSDETLQIMIASMKIKEALPHVPIFDRIYINREYILVLSNKM 385
QY 369 QKIINDNFNDVNFRLIGANVDDMLNTRCRGRVHQNAGNQADN 414
DB 386 QKMVNDNFDDVNFRLIGANVDDMLNTRCRGRVHQNAGNQADN-----ENPDN 421
```


Query Match	Best Local Similarity	Score	DB 1	DB 2	Length	432
Matches	Conservative	63	Mismatches	65	Indels	13
Matches	Conservative	63	Mismatches	65	Indels	13
12	NLAHSMKVIYEWKHIDFPGSDERRDAATKSGFDTHTKYPDPVDRWDRKTFVTLERNNG	71				
26	SLNKSPLPILHEWKFDFDYGSDERRQDAILSGEYDKNNYPDIDQWHDKIPVTLMLRYNG	85				
72	VPSSLVNTNKKGKGLLPYPDPWGFAXYDCSGIVSAFKIADVKFRLWLDLGLVNN	131				
86	VPSSLVNTNKKGKGLLPYPDPWGFAXYDCSGIVSAFKIADVKFRLWLDLGLVNN	145				
132	NQPCSPKLTFLDKTSKLVQVEIPHNTAVNATTGMLVSLAVQADID---RTNMTVYI	188				
146	TQPCSPKLTFLDKTSKLVQVEIPHNTAVNATTGMLVSLAVQADID---RTNMTVYI	205				
189	ADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTAVAGESFTVKNIGCIATSPVTNL	248				
206	ADEKGEGLIVHNSDDSFHRLTSNTFDYDPRYTKLTAVAGESFTVKNIGCIATSPVTNL	265				
249	YSPSLSHGLYYVDTEQFRNPQYEEYVQSGSDILNTQSGKVVKNGVLFLGLVGN	308				
266	YSPVASTSYLYVNTQFRNTQSDIHYEGVQNTIDTQSAKVVSKSGVLFLGLVGD	325				
309	GIACVNEHVLQRESFDVVAQNEETLQIMVSKMIMENLQSGRINDPEGNEYMLALS	368				
326	ALGCWNEHRLERHNTVAQSDDELQIMVSKMIMENLQSGRINDPEGNEYMLALS	385				
369	QKIINDFNFDVNVFRILGANVDDLMRNTCGHYHQNAGNQADN	414				
386	QKVNDFNFDVNVFRILGANVDDLMRNTCGHYHQNAGNQADN	421				

Query Match	Best Local Similarity	Score	DB 1	DB 2	Length	432
Matches	Conservative	63	Mismatches	65	Indels	13
Matches	Conservative	63	Mismatches	65	Indels	13
12	NLAHSMKVIYEWKHIDFPGSDERRDAATKSGFDTHTKYPDPVDRWDRKTFVTLERNNG	71				
26	SLNKSPLPILHEWKFDFDYGSDERRQDAILSGEYDKNNYPDIDQWHDKIPVTLMLRYNG	85				
72	VPSSLVNTNKKGKGLLPYPDPWGFAXYDCSGIVSAFKIADVKFRLWLDLGLVNN	131				
86	VPSSLVNTNKKGKGLLPYPDPWGFAXYDCSGIVSAFKIADVKFRLWLDLGLVNN	145				
132	NQPCSPKLTFLDKTSKLVQVEIPHNTAVNATTGMLVSLAVQADID---RTNMTVYI	188				
146	TQPCSPKLTFLDKTSKLVQVEIPHNTAVNATTGMLVSLAVQADID---RTNMTVYI	205				
189	ADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTAVAGESFTVKNIGCIATSPVTNL	248				
206	ADEKGEGLIVHNSDDSFHRLTSNTFDYDPRYTKLTAVAGESFTVKNIGCIATSPVTNL	265				
249	YSPSLSHGLYYVDTEQFRNPQYEEYVQSGSDILNTQSGKVVKNGVLFLGLVGN	308				
266	YSPVASTSYLYVNTQFRNTQSDIHYEGVQNTIDTQSAKVVSKSGVLFLGLVGD	325				
309	GIACVNEHVLQRESFDVVAQNEETLQIMVSKMIMENLQSGRINDPEGNEYMLALS	368				
326	ALGCWNEHRLERHNTVAQSDDELQIMVSKMIMENLQSGRINDPEGNEYMLALS	385				
369	QKIINDFNFDVNVFRILGANVDDLMRNTCGHYHQNAGNQADN	414				
386	QKVNDFNFDVNVFRILGANVDDLMRNTCGHYHQNAGNQADN	421				

Query Match	Best Local Similarity	Score	DB 1	DB 2	Length	432
Matches	Conservative	63	Mismatches	65	Indels	13
Matches	Conservative	63	Mismatches	65	Indels	13
12	NLAHSMKVIYEWKHIDFPGSDERRDAATKSGFDTHTKYPDPVDRWDRKTFVTLERNNG	71				
26	SLNKSPLPILHEWKFDFDYGSDERRQDAILSGEYDKNNYPDIDQWHDKIPVTLMLRYNG	85				
72	VPSSLVNTNKKGKGLLPYPDPWGFAXYDCSGIVSAFKIADVKFRLWLDLGLVNN	131				
86	VPSSLVNTNKKGKGLLPYPDPWGFAXYDCSGIVSAFKIADVKFRLWLDLGLVNN	145				
132	NQPCSPKLTFLDKTSKLVQVEIPHNTAVNATTGMLVSLAVQADID---RTNMTVYI	188				
146	TQPCSPKLTFLDKTSKLVQVEIPHNTAVNATTGMLVSLAVQADID---RTNMTVYI	205				
189	ADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTAVAGESFTVKNIGCIATSPVTNL	248				
206	ADEKGEGLIVHNSDDSFHRLTSNTFDYDPRYTKLTAVAGESFTVKNIGCIATSPVTNL	265				
249	YSPSLSHGLYYVDTEQFRNPQYEEYVQSGSDILNTQSGKVVKNGVLFLGLVGN	308				
266	YSPVASTSYLYVNTQFRNTQSDIHYEGVQNTIDTQSAKVVSKSGVLFLGLVGD	325				
309	GIACVNEHVLQRESFDVVAQNEETLQIMVSKMIMENLQSGRINDPEGNEYMLALS	368				
326	ALGCWNEHRLERHNTVAQSDDELQIMVSKMIMENLQSGRINDPEGNEYMLALS	385				
369	QKIINDFNFDVNVFRILGANVDDLMRNTCGHYHQNAGNQADN	414				
386	QKVNDFNFDVNVFRILGANVDDLMRNTCGHYHQNAGNQADN	421				

Query Match	
-------------	--

```
QY 354 -----DPEGNEYMALSNRMQKLIIN 374
Db 499 DRMDTMDRTDQGRIDRMDKIDRMDRDTNRMDRMRNMROMNEYMALSMKLOKFINN 558
QY 375 DFNFDVNFRLGANVDDLMRNTRCGRYHNQAGNQADNQADNQADNQADNQADNQADN 429
Db 559 DYNFNEVNFRLGANVDDLMRNTRC-----NSDNQN-NNQNKHN 597

RESULT 13
QSVLE2.APICC
ID QSVLE2.APICC PRELIMINARY; PRT; 433 AA.
AC QSVLE2;
DT 01-FEB-2005 (T-EMBLrel. 29, Created)
DT 01-FEB-2005 (T-EMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE Major royal jelly protein MRJp1.
OS Apis cerana cerana (Oriental honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=94128;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Head;
RA Songkun S., Shenglu C., Stefan A., Boxiong Z.;
RT "Molecular Cloning of MRJp1 cDNA from Apis cerana cerana in China.";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY279539; AAO16677.1; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
SQ SEQUENCE 433 AA; 49045 MW; 86D6C115EF40B9B5 CRC64;

Query Match 50.2%; Score 1403.5; DB 2; Length 433;
Best Local Similarity 67.3%; Pred. No. 1.3e-80;
Matches 269; Conservative 52; Mismatches 75; Indels 3; Gaps 1;

QY 12 NLAHSMKVIYEWKHIDPFGSDERRDAAIKSGEFDHTKYNPPFDVDRWRDKTFVTIERNG 71
Db 27 SLNKSLSVLHEWKFFDYDFDSERRQDAILSGEYDYRKYNPSPVDQWHGKIFVTMLRYNG 86
QY 72 VPSLNVVTKKGKGGPPLLAPYDPSFAKYDCSGIVSAFKIADVDFDLWLVDLSGLVNN 131
Db 87 VPSLNVISKIGDGGPQLQYPDWSFAKYDDCSGIVSATKLAIDKCDRLWLVDLSGLVNN 146
QY 132 NOPMCPKLLTFLDKTSKLKQVEIPHNIAVNATTGKGLVSLAVQAID---RTNTMVYI 188
Db 87 VPSLNVISKIGDGGPQLQYPDWSFAKYDDCSGIVSATKLAIDKCDRLWLVDLSGLVNN 146
QY 147 TQPMCSPKLLTFLDTLSQLLKQVEIPHDVAVNATTGKRLSSLAQVPLDCNNGDTMVYI 206
Db 132 NOPMCPKLLTFLDKTSKLKQVEIPHNIAVNATTGKGLVSLAVQAID---RTNTMVYI 188
QY 189 ADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTAVGESFTVKNGICGIALSPVTNNL 248
Db 147 TQPMCSPKLLTFLDTLSQLLKQVEIPHDVAVNATTGKRLSSLAQVPLDCNNGDTMVYI 206
QY 189 ADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTAVGESFTVKNGICGIALSPVTNNL 248
Db 207 ADEKGEGLIVYHSDSDSFHRLTSKTFDYDPKFTKMTINGESFTTQSGISGMALSPMTNNL 266
QY 189 ADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTAVGESFTVKNGICGIALSPVTNNL 248
Db 207 ADEKGEGLIVYHSDSDSFHRLTSKTFDYDPKFTKMTINGESFTTQSGISGMALSPMTNNL 266
QY 249 YYSPLSHGLIYYVDTRQFRNPQVEENNVQEGSQDILNTQSGFKVYSKNGVLFGLVGN 308
Db 249 YYSPLSHGLIYYVDTRQFRNPQVEENNVQEGSQDILNTQSGFKVYSKNGVLFGLVGN 308
QY 267 YYSFVASTLSYYVNTQFRTSNTEQNAVHVEGVQNLDTQSSAKVYKSGVLFGLVGD 326
Db 267 YYSFVASTLSYYVNTQFRTSNTEQNAVHVEGVQNLDTQSSAKVYKSGVLFGLVGD 326
QY 309 GIACVNEHVOVLRSPDVVAQNEETLQIMVSMKIMENLPQSGRINDEPGEYNEMLALSNRM 368
Db 309 GIACVNEHVOVLRSPDVVAQNEETLQIMVSMKIMENLPQSGRINDEPGEYNEMLALSNRM 368
QY 327 ALGCWNEHRSLEHRTVIRTAQSDETLQIMVGMKIKALPHVPIFDRIYINREYLIVLSNRM 386
Db 327 ALGCWNEHRSLEHRTVIRTAQSDETLQIMVGMKIKALPHVPIFDRIYINREYLIVLSNRM 386
QY 369 QKIINDFNFNDVNFRLGANVDDLMRNTRCGRYHNQ 406
Db 327 ALGCWNEHRSLEHRTVIRTAQSDETLQIMVGMKIKALPHVPIFDRIYINREYLIVLSNRM 386
QY 369 QKIINDFNFNDVNFRLGANVDDLMRNTRCGRYHNQ 406
Db 387 QKMANNDYFNDFNFRIMDANVNDLILNTRCENPNNDN 424

RESULT 14
Q8MMJ1.APICE
ID Q8MMJ1.APICE PRELIMINARY; PRT; 433 AA.
AC Q8MMJ1;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
```

```
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Major royal jelly protein MRJp1 precursor (Major royal jelly protein
DE 1).
GN Name=MRJp1; Synonyms=mrjpl;
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Nurse heads;
RA Sittipraneed S., Imjongjirak C.;
RT "Molecular Cloning of Major Royal Jelly Protein (MRJp1) cDNA from Apis
RT cerana in Thailand.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Imjongjirak C., Klinbunga S., Sittipraneed S.;
RT "Cloning, Expression and Genomic Organization of Genes Encoding Major
RT Royal Jelly Protein 1 and 2 of the Honeybee (Apis cerana).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF525776; AAM88281.2; -; mRNA.
DR EMBL; AY515688; AAS889556.1; -; Genomic_DNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW SIGNAL.
FT SIGNAL 1 20 Potential.
SQ SEQUENCE 433 AA; 48969 MW; PEC24D6A4BC7BF2F CRC64;

Query Match 50.2%; Score 1402.5; DB 2; Length 433;
Best Local Similarity 67.1%; Pred. No. 1.5e-80;
Matches 267; Conservative 54; Mismatches 74; Indels 3; Gaps 1;

QY 12 NLAHSMKVIYEWKHIDPFGSDERRDAAIKSGEFDHTKYNPPFDVDRWRDKTFVTIERNG 71
Db 27 SLNKSLSVLHEWKFFDYDFDSERRQDAILSGEYDYRKYNPSPVDQWHGKIFVTMLRYNG 86
QY 72 VPSLNVVTKKGKGGPPLLAPYDPSFAKYDCSGIVSAFKIADVDFDLWLVDLSGLVNN 131
Db 87 VPSLNVISKIGDGGPQLQYPDWSFAKYDDCSGIVSATKLAIDKCDRLWLVDLSGLVNN 146
QY 132 NOPMCPKLLTFLDKTSKLKQVEIPHNIAVNATTGKGLVSLAVQAID---RTNTMVYI 188
Db 147 TQPMCSPKLLTFLDTLSQLLKQVEIPHDVAVNATTGKRLSSLAQVPLDCNNGDTMVYI 206
QY 189 ADEKGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTAVGESFTVKNGICGIALSPVTNNL 248
Db 207 ADEKGEGLIVYHSDSDSFHRLTSKTFDYDPKFTKMTINGESFTTQSGISGMALSPMTNNL 266
QY 249 YYSPLSHGLIYYVDTRQFRNPQVEENNVQEGSQDILNTQSGFKVYSKNGVLFGLVGN 308
Db 267 YYSFVASTLSYYVNTQFRTSNTEQNAVHVEGVQNLDTQSSAKVYKSGVLFGLVGD 326
QY 309 GIACVNEHVOVLRSPDVVAQNEETLQIMVSMKIMENLPQSGRINDEPGEYNEMLALSNRM 368
Db 327 ALGCWNEHRSLEHRTVIRTAQSDETLQIMVGMKIKALPHVPIFDRIYINREYLIVLSNRM 386
QY 369 QKIINDFNFNDVNFRLGANVDDLMRNTRCGRYHNQ 406
Db 387 QKMANNDYFNDFNFRIMDANVNDLILNTRCENPNNDN 424

RESULT 15
Q6QNI6.APICE
ID Q6QNI6.APICE PRELIMINARY; PRT; 485 AA.
AC Q6QNI6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Major royal jelly protein MRJp4 precursor.
```


This Page Blank (upper)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:09:24 ; Search time 56.6049 Seconds
(without alignments)
765.341 Million cell updates/sec

Title: US-10-525-567-3
Perfect score: 2796
Sequence: 1 AAVNHORKSANNLAHSMKVI.....NNQNDNRNDNQVHSSKLH 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5 COMB.pap.*
2: /cgm2_6/ptodata/1/iaa/6 COMB.pap.*
3: /cgm2_6/ptodata/1/iaa/H COMB.pap.*
4: /cgm2_6/ptodata/1/iaa/PTUS COMB.pap.*
5: /cgm2_6/ptodata/1/iaa/RE COMB.pap.*
6: /cgm2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	247	8.8	1584	2	US-09-457-040B-27
2	232	8.3	162	2	US-09-270-767-33773
3	232	8.3	162	2	US-09-270-767-48990
4	220	7.9	954	2	US-09-570-856B-31
5	206	7.4	524	2	US-09-543-681A-4787
6	198.5	7.1	418	2	US-09-248-796A-20578
7	194.5	7.0	802	2	US-09-134-000C-5150
8	193	6.9	2391	1	US-08-446-855A-2
9	193	6.9	2391	2	US-09-150-741-2
10	182	6.5	961	2	US-09-487-558B-132
11	180	6.4	182	2	US-09-583-110-4334
12	180	6.4	186	2	US-09-107-433-3319
13	176	6.3	174	2	US-09-134-001C-4460
14	172.5	6.2	1162	1	US-08-728-323A-2
15	172.5	6.2	1162	2	US-09-298-568-2
16	172.5	6.2	1162	2	US-09-410-399-2
17	172.5	6.2	1162	2	US-09-894-273-2
18	169	6.0	666	2	US-09-487-558B-36
19	168.5	6.0	2184	2	US-09-417-485D-6
20	167.5	6.0	467	2	US-09-134-001C-3235
21	167.5	6.0	472	2	US-09-710-279-1902
22	166.5	6.0	696	2	US-09-248-796A-14133
23	163.5	5.8	110	1	US-08-569-166-34
24	163.5	5.8	133	2	US-09-710-279-1924
25	162.5	5.8	826	1	US-07-638-431-2
26	162.5	5.8	826	4	PCT-US92-00018-2
27	162	5.8	369	2	US-09-248-796A-23009

28	157.5	5.6	188	2	US-09-248-796A-21795	Sequence 21795, A
29	157.5	5.6	430	1	US-08-945-848-8	Sequence 8, Appli
30	156.5	5.6	213	2	US-09-248-796A-18858	Sequence 18858, A
31	155	5.5	263	2	US-09-248-796A-15305	Sequence 15305, A
32	154.5	5.5	1259	2	US-09-949-016-10366	Sequence 10366, A
33	148.5	5.3	758	2	US-09-487-558B-224	Sequence 224, App
34	147	5.3	124	2	US-09-248-796A-21892	Sequence 21892, A
35	146.5	5.2	596	2	US-09-752-165-2	Sequence 2, Appli
36	146.5	5.2	596	2	US-10-167-831-2	Sequence 2, Appli
37	145.5	5.2	502	2	US-09-248-796A-19204	Sequence 19204, A
38	145	5.2	3788	2	US-09-336-447A-76	Sequence 76, Appl
39	145	5.2	3788	2	US-09-952-267B-76	Sequence 76, Appl
40	144	5.2	1195	2	US-09-538-092-517	Sequence 517, App
41	143	5.1	588	2	US-09-248-796A-20839	Sequence 20839, A
42	143	5.1	657	2	US-09-248-796A-27210	Sequence 27210, A
43	143	5.1	1588	4	PCT-US93-07261-11	Sequence 11, Appl
44	143	5.1	1663	4	PCT-US93-07261-16	Sequence 16, Appl
45	142.5	5.1	78	2	US-09-328-352-6915	Sequence 6915, Ap

ALIGNMENTS

RESULT 1
US-09-457-040B-27
; Sequence 27, Application US/09457040B
; Patent No. 6387641
; GENERAL INFORMATION:
; APPLICANT: Vertex Pharmaceuticals Incorporated
; APPLICANT: Bellon, Steve
; TITLE OF INVENTION: Crystallized P38 Complexes
; FILE REFERENCE: VPI/98-14
; CURRENT APPLICATION NUMBER: US/09/457,040B
; CURRENT FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1584
; TYPE: PRT
; ORGANISM: DICTDI - Dictyostelium Discoideum
US-09-457-040B-27

Query Match	8.8%;	Score 247;	DB 2;	Length 1584;
Best Local Similarity	24.7%;	Pred. No. 1.5e-14;		
Matches	74;	Conservative	30;	Mismatches 108; Indels 88; Gaps 9;
Qy	255	SHGLYYVDTEQFRNPQYEENNVQEGSQDILNTQSFQKVSQKGVFLGLVGN-	-----	308
Db	295	SYGVHDDGRKFR---WREBPGVNEG-----BSYGSYKKGDIIGCLSFSTRIFFT	344	
Qy	309	-----GIACVNEHVLQRESFDVVAQNEETLQIVSMKIMENLPQSGRINDPEGNYML	362	
Db	345	KNGMYLTAFSNVYGVF-----YPSVAFNEPGISI-----TGVFQPP-----	381	
Qy	363	ALSNRMQKIINDPNDVNFRIILGANVDDILMRNCRGYHQNAGNQADNQADNQNA	422	
Db	382	-----PKFSQVTLMLKNVNSTIL-----VPGNNNNNNNNNNNNNNNN	419	
Qy	423	N-----NQADNQANKQNGRQNDNRQNDKQNGRQNDKQNGRQNDKQNGRQNDKQNG	462	
Db	420	NIIGNGKITTTTSTSPSSINNNDISSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	479	
Qy	463	NRQNDKQNGRQNGKQNDKQNGRQNDKQNGRQNDKQNGRQNDKQNGRQNDKQNGRQNDKQNG	522	
Db	480	NSSNTNNNNNTTT-NNNNNSNNNNNNNNNSNSNNNNNNNNNNNNNNNNNNNNNNNNNN	538	

RESULT 2
US-09-270-767-33773
; Sequence 33773, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.

```
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33773
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33773

Query Match
Best Local Similarity 8.3%; Score 232; DB 2; Length 162;
Matches 52; Conservative 25; Mismatches 43; Indels 18; Gaps 5;

Qy 44 EFQHTKNYPFDVDRWRDKTFTVIER--NNGVPSILNVVT--NKGKGGPLLRPYPDWSF--- 98
Db 7 DFVPKNNLPGLGIDVHNNRLFVTTFRWKNVGPASLGLTPFPSPKGVKGPKALPYPNWEAHGN 66

Qy 99 AKYEDCSGIVSAFKIAVDKFDRLWLVDLSGLVN---NNQPMCSPKLLTFDLKTSKL----- 150
Db 67 PNNPDCSKLSVYRTAVDRCDRIWLIDSGIVGNATINLQICPKPIVYVDLKSDELIVRYN 126

Qy 151 -----VKQVEIPHNIAYN 163
Db 127 LEASHVKQDSLHSGNIVVD 144

RESULT 3
US-09-270-767-48990
; Sequence 48990, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48990
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48990

Query Match
Best Local Similarity 8.3%; Score 232; DB 2; Length 162;
Matches 52; Conservative 25; Mismatches 43; Indels 18; Gaps 5;

Qy 44 EFQHTKNYPFDVDRWRDKTFTVIER--NNGVPSILNVVT--NKGKGGPLLRPYPDWSF--- 98
Db 7 DFVPKNNLPGLGIDVHNNRLFVTTFRWKNVGPASLGLTPFPSPKGVKGPKALPYPNWEAHGN 66

Qy 99 AKYEDCSGIVSAFKIAVDKFDRLWLVDLSGLVN---NNQPMCSPKLLTFDLKTSKL----- 150
Db 67 PNNPDCSKLSVYRTAVDRCDRIWLIDSGIVGNATINLQICPKPIVYVDLKSDELIVRYN 126

Qy 151 -----VKQVEIPHNIAYN 163
Db 127 LEASHVKQDSLHSGNIVVD 144

RESULT 4
US-09-570-856B-31
; Sequence 31, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Basil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RPT/RMS/RMK
```

```
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 954
; TYPE: PRT
; ORGANISM: Ruminococcus flavefaciens
US-09-570-856B-31

Query Match
Best Local Similarity 7.9%; Score 220; DB 2; Length 954;
Matches 67; Conservative 26; Mismatches 44; Indels 50; Gaps 12;

Qy 365 SNRMQKIIINDFN--PNDVNERILGANVVDLMDRTTCGRYHQNAGNQAD-----NQNA 417
Db 415 NNNQQQ--NNDWNQNNQNNN-----NNQQQNDNDWNNNQ--GQQNDNDWNNQNN 464

Qy 418 DNQANNNQNA-----DNQANQKQNGRQNDNRQNDNK---QNGNRQNDNRQNDNK----- 461
Db 465 WQNNNNQNAWGDWNNNNWQNDQNNQNNQNNQNNQNTWQNNQNNQNNQNNQNDWNNQNN 524

Qy 462 -GNRQND-----NKQNGNRQNG---NKQNDKQNGRQND-----DNKRGNR---QNDNQ 504
Db 525 QGQQQNDNDWNNQNNQNNQNGWNNQNNQNNQNNQNNQNAWGDWNNNNQNNQNGQNDNW 584

Qy 505 NNQNDNN 511
Db 585 NNOQQNN 591

RESULT 5
US-09-543-681A-4787
; Sequence 4787, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4787
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4787

Query Match
Best Local Similarity 7.4%; Score 206; DB 2; Length 524;
Matches 65; Conservative 23; Mismatches 74; Indels 26; Gaps 10;

Qy 338 VSMKIMENLPQSGRINDPGEYMLALSNRMQK-----IINNDNFNFDVNFRIILGANVDDL 393
Db 141 IALKCLYEKLDKNELDNQIFAEIYIELDNKRSGEIDLKNSFNQVNFSAIRQLVSKA 200

Qy 394 MRNTRCGRYHQNAGNQADNQADNQANQANQANQANQANQANQANQANQANQANQANQAN 453
Db 201 IEN-----DNTWLDTEN-DNINLENDNINLEN-DNINLENDNINLENDNINLEN-DNIN 251

Qy 454 RQNDN-----KQNGNRQNDKQNGRQNDKQNGRQNDKQNGRQNDKQNGRQNDKQNGRQND 509
Db 252 LENDNINLENDNINLENDN--VNLENDNVLENDNV---NLENDNV---NLENDNVLEND 304

Qy 510 --NNRNDN 515
Db 305 NINLENDN 312
```

RESULT 6
 US-09-248-796A-20578
 ; Sequence 20578, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 20578
 ; LENGTH: 418
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-248-796A-20578

Query Match 7.1%; Score 198.5; DB 2; Length 418;
 Best Local Similarity 25.1%; Pred. No. 1e-10;
 Matches 67; Conservative 53; Mismatches 98; Indels 49; Gaps 12;

QY 268 NPOYENNVOYEGSODILNTOSFGKVKSGKGLFGLVGNSGIACVNEHQVLORESFDVV 327
 DB 175 NSSFDEDTLLI-NSPDLNENQNFVTHSTSG-----SATPNSNSHS-LQSKKKNY 223
 QY 328 AQNBETLQMIYSKMIMENLPQSGRINDPEGNEYMALSNRMQKI-----INND 375
 DB 224 KRNLSILKELPPI-ILENVP-SSLPKKQPVNNLINIPKARSKENTPPTTPROFTNHND 281
 QY 376 FNFNDVNPRIIGANVDDLLMRNTRCGRVHNQAGNQADNQADNQADNQADNQADNQANKQ 435
 DB 282 F---EVTHQWGN-----NINHRNNSVDSRSDNGQHRNNSYDSRSDHQ 326
 QY 436 NGNQRNDNRQNDNQNGNRQNDNQNGNRQNDN--KQNGNRQNGKQNDNQNGNRQNDN 493
 DB 327 --HRRQPSQQNNYNNNNNNNNNNNNNNNNNNNNNNNGFVGRSGSVRVNNYNNNN--NGNANNNG 382
 QY 494 KRNGN---RQNDNQNGNDNRNDNQV 517
 DB 383 NNHGKFKRRSTYNNNNNNNNNNNNNNNNNNNNNNKRNSQL 409

RESULT 7
 US-09-134-000C-5150
 ; Sequence 5150, Application US/09134000C
 ; Patent No. 6617156
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 032796-032
 ; CURRENT APPLICATION NUMBER: US/09/134,000C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/055,778
 ; PRIOR FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 6812
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5150
 ; LENGTH: 802
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis
 US-09-134-000C-5150

Query Match 7.0%; Score 194.5; DB 2; Length 802;
 Best Local Similarity 38.3%; Pred. No. 7.4e-10;
 Matches 49; Conservative 13; Mismatches 45; Indels 21; Gaps 6;

```
Db 1277 NH-----LYNEVDDKDTQLHKNNNNNM-----NSGVNCKLKNESYG 1318
Qy 218 PRYKLTVAGESFTVKGIC-GIALS---PVTNNLYSPLS-----SH 256
Db 1319 YNNSNCINTNNIENNICHDISINKNIKVTIINNNSISNNENVTNLNCVSRAGSH 1378
Qy 257 GLYYVDTQFRNPQYBENNVOYEGSQD--ILNTQSFQKVVSKNGVLFLGLVNGSGIACVN 314
Db 1379 HIY-----GKEEKSI---GSDDTNILSAQN-----SNNNFSCNN 1409
Qy 315 EH-----QVLQ-----RESFDVVAQNEETLQMTIVSMKIMENLPQSGRINDPEGNEYM 361
Db 1410 ENMNKANVDVNLNDTKKREDINTTTVFMEGQNSVINNNKEN-----SSLLKGDEEDIVM 1466
Qy 362 LAL--SNRMQKIINN-----DFNFNDVN-----FRILGAN---VDDLNRNT--- 397
Db 1467 VNLKKNYNSVINNVDCRKKDMDGKNIINDECKTYKKNYKDKMGLNINIVDLSNGTSHS 1526
Qy 398 -----RCGRYHNQVAGN-----Q 410
Db 1527 TNDHLYLDNFTSDIEIGNNKNDMYLSKEKSI-SNKNPGNSYYVVDVSVYNNYKINKMKE 1586
Qy 411 NADQNADQNANQNADQNANKQ-----NGNRQNDNRND-----NKONGN 453
Db 1587 LIDNENLNDYNNNNVNNCSNYNNASAFVNGKDRNDNLENDCKIEKMDHTYKHYNRLN-N 1645
Qy 454 RQNDNKQ-----GNRQNDNKQNRQNG-NKQN--DNKQNGRQNDNKRNGRQNDQNN 506
Db 1646 RRTSTERNMLMVNNEKSNHEKGHRRLNGLNKKNEKMKKGNKDKKNYHYVNHKRN 1705
Qy 507 QNDNRNDNQVHH 519
Db 1706 EYNSNNIESKFNN 1718
```

RESULT 9

```
US-09-150-741-2
; Sequence 2, Application US/09150741
; Patent No. 6183996
; GENERAL INFORMATION:
; APPLICANT: Stewart et al.
; TITLE OF INVENTION: Nucleotide Sequence Encoding Carbanoyl Phosphate
; Patent No. 6183996
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/150,741
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PL6380
; EARLIER FILING DATE: 1992-12-16
; EARLIER APPLICATION NUMBER: AU93/00617
; EARLIER FILING DATE: 1993-12-02
; EARLIER APPLICATION NUMBER: 08/446,855
; EARLIER FILING DATE: 1995-07-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2391
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: protein
US-09-150-741-2
```

```
Query Match 6.9%; Score 193; DB 2; Length 2391;
Best Local Similarity 19.8%; Pred No. 6.4e-09;
Matches 133; Conservative 106; Mismatches 204; Indels 230; Gaps 33;

Qy 5 HORKSANNLAHSMKVIYEWKHIDPDF-----GSDERRDAAIKSGEFDHTKNYFVDV 55
Db 1118 HQ---AFHLNMPMDKIHLTHIDWFLHFKFYNIYLNQNLKLTLEQLSFNDLKY--FKK 1172
Qy 56 DRWRDK-----TPVTIERNNGVP--SSLVNVTNKKGGGFLLRPPYDPWDSFAKYEDCSGI 107
```

```
Db 1173 HGFSDKQIAHYLSFNTSDNNNNNNNNISRCVTEN-----DVMKYREKGL 1217
Qy 108 VSAFKIADKDF-----DRLWLDGSLVNNQNP--MCSPKLLTPDLTKTSKLIVKQVEIP 157
Db 1218 FPHIKV-IDTLSAEPALTNLYLYTYQGQHDVPLPLNMRKKICTILNNKRNANKKHHVK 1276
Qy 158 HNIAVNATTMGELYSLAVQAIDRTNTWYIADKEGGLIMYQNSDDSFHRLTSNFTDYD 217
Db 1277 NH-----LYNEVDDKDTQLHKNNNNNM-----NSGVNCKLKNESYG 1318
Qy 218 PRYKLTVAGESFTVKGIC-GIALS---PVTNNLYSPLS-----SH 256
Db 1319 YNNSNCINTNNIENNICHDISINKNIKVTIINNNSISNNENVTNLNCVSRAGSH 1378
Qy 257 GLYYVDTQFRNPQYBENNVOYEGSQD--ILNTQSFQKVVSKNGVLFLGLVNGSGIACVN 314
Db 1379 HIY-----GKEEKSI---GSDDTNILSAQN-----SNNNFSCNN 1409
Qy 315 EH-----QVLQ-----RESFDVVAQNEETLQMTIVSMKIMENLPQSGRINDPEGNEYM 361
Db 1410 ENMNKANVDVNLNDTKKREDINTTTVFMEGQNSVINNNKEN-----SSLLKGDEEDIVM 1466
Qy 362 LAL--SNRMQKIINN-----DFNFNDVN-----FRILGAN---VDDLNRNT--- 397
Db 1467 VNLKKNYNSVINNVDCRKKDMDGKNIINDECKTYKKNYKDKMGLNINIVDLSNGTSHS 1526
Qy 398 -----RCGRYHNQVAGN-----Q 410
Db 1527 TNDHLYLDNFTSDIEIGNNKNDMYLSKEKSI-SNKNPGNSYYVVDVSVYNNYKINKMKE 1586
Qy 411 NADQNADQNANQNADQNANKQ-----NGNRQNDNRND-----NKONGN 453
Db 1587 LIDNENLNDYNNNNVNNCSNYNNASAFVNGKDRNDNLENDCKIEKMDHTYKHYNRLN-N 1645
Qy 454 RQNDNKQ-----GNRQNDNKQNRQNG-NKQN--DNKQNGRQNDNKRNGRQNDQNN 506
Db 1646 RRTSTERNMLMVNNEKSNHEKGHRRLNGLNKKNEKMKKGNKDKKNYHYVNHKRN 1705
Qy 507 QNDNRNDNQVHH 519
Db 1706 EYNSNNIESKFNN 1718

RESULT 10
US-09-487-558B-132
; Sequence 132, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 132
; LENGTH: 961
; TYPE: PRT
```



```

THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3319:
SEQUENCE CHARACTERISTICS:
LENGTH: 186 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...186
SEQUENCE DESCRIPTION: SEQ ID NO: 3319:
US-09-107-433-3319

Query Match          6.4%; Score 180; DB 2; Length 186;
Best Local Similarity 33.3%; Pred. No. 1.8e-09;
Matches 54; Conservative 27; Mismatches 49; Indels 32; Gaps 10

QY      393 LMRNTTCGRHYQNAG----NQAD--NQADNQNAN--NQADNQ-----ANKQNGNRQN 441
DB      14 LLQNCVQCNVLNQRNLNRSWKNQQLNRNKNQGNQRLNRSRKKNQQLNRSRKKNQQLN 73

QY      442 DNFRQNDNKO--NGNRQNDNKO--NGNRQNDN-----KQNGNRQNGKQNDNKQ--NGNRQN 491
DB      74 RSKNQQLRNLRSRKKNQQLNRSLNRKNQQLNRSLNRKNQQLNRSLNRKNQQLNRSLNR 133

QY      492 DNKR-----NGNRQNDNQND-----NNRNNDNVHHRSK 522
DB      134 QNQLNRSLNRKNQQLRNLNRNKNQGNQRLNRNKNQGNQIASHK 175

RESULT 13
US-09-134--001C-4460
Sequence 4460, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964

```

```

Best Local Similarity 29.2%; Pred.No. 2.1e-07;
Matches 33; Conservative 20; Mismatches 59; Indels 1; Gaps 1;

QY 405 QNAGNQADNQADNQANNNQADNQAN- KQNGNRQNDNRQNDNKQNGNRQNDNKQNGN 463
Db 600 QQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDE 659

QY 464 RQNDKQNGNRQNGKQNDKQNGNRQNDKQNGNRQNDKQNGNRQNDKQNGNRQNDNQ 516
Db 660 QQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQ 712

RESULT 15
US-09-298-568-2
; Sequence 2, Application US/09298568
; Patent No. 6322792
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Ballestas, Mary E.
; APPLICANT: Kaye, Kenneth M.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US/09/298,568
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,422
; EARLIER FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-2

Query Match 6.2%; Score 172.5; DB 2; Length 1162;
Best Local Similarity 29.2%; Pred.No. 2.1e-07;
Matches 33; Conservative 20; Mismatches 59; Indels 1; Gaps 1;

QY 405 QNAGNQADNQADNQANNNQADNQAN- KQNGNRQNDNRQNDNKQNGNRQNDNKQNGN 463
Db 600 QQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDE 659

QY 464 RQNDKQNGNRQNGKQNDKQNGNRQNDKQNGNRQNDKQNGNRQNDKQNGNRQNDNQ 516
Db 660 QQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQ 712

Search completed: May 3, 2006, 19:12:03
Job time : 58.6049 secs

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:10:39 ; Search time 183.831 Seconds
(without alignments)
1190.997 Million cell updates/sec

Title: US-10-525-567-3

Perfect score: 2796

Sequence: 1 AAVNHQKSNLHAKMKVI.....NNQNDNRNDNQVHSSKLH 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp:*
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:*
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp:*
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp:*
5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp:*
6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	427	15.3	541	6	US-11-097-143-7173	Sequence 7173, Ap
2	422.5	15.1	426	6	US-11-097-143-25233	Sequence 25233, A
3	418.5	15.0	453	6	US-11-097-143-40164	Sequence 40164, A
4	415.5	14.9	412	6	US-11-097-143-20991	Sequence 20991, A
5	408.5	14.6	415	6	US-11-097-143-20973	Sequence 20973, A
6	408.5	14.6	438	6	US-11-097-143-7005	Sequence 7005, Ap
7	320	11.4	429	6	US-11-097-143-28038	Sequence 28038, A
8	319.5	11.4	409	6	US-11-097-143-25236	Sequence 25236, A
9	302.5	10.8	379	6	US-11-097-143-41712	Sequence 41712, A
10	296.5	10.6	1123	5	US-10-287-436A-285	Sequence 285, App
11	294.5	10.5	316	6	US-11-097-143-1674	Sequence 1674, Ap
12	281	10.1	530	6	US-11-097-143-42198	Sequence 42198, A
13	279.5	10.0	638	5	US-10-732-923-9918	Sequence 9918, Ap
14	267	9.5	2150	4	US-10-135-322-17	Sequence 17, Appl
15	251	9.0	6761	5	US-10-732-923-15035	Sequence 15035, A
16	247	8.8	568	4	US-10-086-510-5	Sequence 5, Appl
17	247	8.8	1584	5	US-10-732-923-13548	Sequence 13548, A
18	237	8.5	1895	6	US-11-097-143-37056	Sequence 37056, A
19	236	8.4	1331	4	US-10-087-464-50	Sequence 50, Appl
20	232.5	8.3	1213	5	US-10-732-923-12952	Sequence 12952, A
21	231.5	8.3	3328	5	US-10-732-923-8311	Sequence 8311, Ap
22	227.5	8.1	393	6	US-11-097-143-699	Sequence 699, App
23	226.5	8.1	436	5	US-10-732-923-19248	Sequence 19248, A
24	226.5	8.1	611	4	US-10-086-510-4	Sequence 4, Appl
25	223.5	8.0	123	4	US-10-437-963-109658	Sequence 109658, A
26	217	7.8	382	6	US-11-097-143-32673	Sequence 32673, A
27	214	7.7	2964	5	US-10-732-923-13552	Sequence 13552, A

ALIGNMENTS

RESULT 1

US-11-097-143-7173

; Sequence 7173, Application US/11097143

; Publication No. US20050208558A1

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig

; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; TITLE OF INVENTION: DROSOPHILA GENES.

; FILE REFERENCE: CL000728

; CURRENT APPLICATION NUMBER: US/11/097,143

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: 60/160,191

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: 60/161,932

; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/173,383

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/184,831

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/191,637

; PRIOR FILING DATE: 2000-03-23

; NUMBER OF SEQ ID NOS: 43008

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7173

; LENGTH: 541

; TYPE: PRF

; ORGANISM: DROSOPHILA

US-11-097-143-7173

Query Match 15.3%; Score 427; DB 6; Length 541;

Best Local Similarity 28.0%; Pred. No. 3.2e-26;

Matches 116; Conservative 85; Mismatches 165; Indels 48; Gaps 13;

Qy 14 AHSMKVYEWKHIDFGSDERRDAAIKSGFDTHTKYNFPDVRDKTFVTIER-NGGV 72

Db 22 AYKLEQRYMSQLDFAPFNTLRKQALASGDYIFQNALPVGVEHFGNLFVTPVRWDGI 81

Qy 73 PSSLNVT-NKKGGKGLLRYPDWSFAYEDC-SGIVSAFKIADVDFRLWLDSGLV- 129

Db 82 PATLTYINMDSLTCGSPDLIPYDWRNSNTAGDCANSITATYRIKVDCEGRWLWLTGTVG 141

Qy 130 -NNNQPMCSPKLLTFDLTKSLVKQVEIPHNIAVNATTGMGELVSLAVQAID----RTN 183

Sequence 15036, A
Sequence 3351, Ap
Sequence 25230, A
Sequence 13547, A
Sequence 13550, A
Sequence 12547, A
Sequence 9614, Ap
Sequence 256, App
Sequence 30, Appl
Sequence 201278,
Sequence 109, App
Sequence 15009, A
Sequence 8438, Ap
Sequence 2, Appl
Sequence 2998, Ap
Sequence 9, Appl
Sequence 9799, Ap
Sequence 33, Appl

Db 142 IGNTTNPCCYAVNVFDTTDRIRRYELP-GVDTNPTNTFIAMI-----AVDIGKNCDD 194
QY 184 TMVYIADEKEGLIMYQNSDDSFHRLTSNTFDY-DPRYTKLTVAGSFYVKNIGICGIAL 241
Db 195 AYAFADDELGYGLIAYSWELNKSWSAHSYFPDPDLRGDPNVAGINFQWGESIGFMSL 254
QY 242 SPVNTN----LYYSPSSHGLYYVDTEQFRNPQVEENNVOYEGSQDIL-----NTQSF 290
Db 255 SPIRSDGYRTLYRSPASHRQFAVSTRILRDETREDSY-----HDFVALDERGPNSHTT 309
QY 291 GKUVSKNGVLFLGLVNGSGIACVNEHQVLORESFDVVAQNEETLQMLVSKIMENLPQSG 350
Db 310 SRVMSDDGIELFLIDQAVGCVHSSMPSPQFHGIVDRDDVGLVFPADVKIDE----- 363
QY 351 RINDPGEYMLALSNNRQKIIINDFNFNDVNFRIILCANVDDLMRNTRCGRYHN 404
Db 364 -----NKNVWVLSRMPVFLSLDDYSNTNFIYTAPLATLIENTVCDLRNN 410

RESULT 2

US-11-097-143-25233
; Sequence 25233, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25233
; LENGTH: 426
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-25233

Query Match 15.1%; Score 422.5; DB 6; Length 426;
Best Local Similarity 26.2%; Pred. No. 5.4e-26;
Matches 111; Conservative 83; Mismatches 155; Indels 75; Gaps 13;
QY 19 VIYEWKHIDPFGSDERRDAAIKSGDFDHTKNTYFPDVRW-----RDKTFVVTIER-NNG 71
Db 34 IVFENKLNQYFFSEQRDQVLRNGRYNPSPIIDIVVYPNGGPPRHFTVTSRFGQ 93
QY 72 VPSLNVVTKKGGKGLLPRLPYR--DWSFAKYEDCSGIVSAFKIADVDFRLVLSGLV 129
Db 94 VPFSGLGVTVTVQRENGSEIOAYFSYQWHSHGANCGLTSSVYRVHIDACQMWVLSGEI 153
QY 130 NNNQPMCSKLLTFLDKTSKLVQVEIPHNIATNATGMGELVSLVAQIAIDR-----TN 183
Db 154 EFVQ-HCAPQVMVFDLATDQLIHRYLPE---TSYKAKVSFRFVNIFADIRDPSPGCKD 209

QY 184 TMVYIADEKEGLIMYQNSDDSFHRLTSNTFDY-DPRYTKLTVAGSFYVKNIGICGIALS 242
Db 210 VFAYLADPTSKAIVVVDVVGQSSWRI-ENKFTYPDAKFGTHTVAGESFELLDGFLALATT 268
QY 243 P-----VTNNLYYSPSSHGLYYVDTEQFRNPQVEENNVOYEGSQDILNT----- 287
Db 269 FLGLGRRLHIFALS-----NELELAIPDLINNATNWKQGLSSS 309
QY 288 -----QSPGKVVSKNGVLFLGLVNGSGIACVNEHQVLORESFDVVAQNEETLQ 335
Db 310 LSEFTVLGKRGICASHAISROGFLFCGFLPIGIFGWDIRRPYNNRENVKLLAINPATLQ 369
QY 336 MIVSKIMENLPQSGRINDPGEYMLALSNNRQKIIINDFNFNDVNFRIILCANVDDLMR 395
Db 370 FVSGMKIVRR-PADGR-----EELWLLSLDRLOKIFAGTIDYREINRYVMRCDVDDLQ 421
QY 396 NTRC 399
Db 422 GRCC 425

RESULT 3

US-11-097-143-40164
; Sequence 40164, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40164
; LENGTH: 453
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-40164

Query Match 15.0%; Score 418.5; DB 6; Length 453;
Best Local Similarity 27.9%; Pred. No. 1.3e-25;
Matches 122; Conservative 84; Mismatches 194; Indels 37; Gaps 12;
QY 16 SMKVIYEWKHIDPFGSDERRDAAIKSGDFDHTKNTYFPDVRWRDKTFVVTIER-NNGVPS 74
Db 21 NLRVAYEWREMDPKYANPDQWSAIERGEFKPANVIPFGLVAGHRLFTLPRWRDGVPA 80
QY 75 SLNVV-TNKKGGKGLLPRLPYRDPWSFAKYEDCS-GIVSAFKIADVDFRLVWLD---SGLV 129
Db 81 SLAYLDLNTSSKGPALKPFPSPQAHNLOEAPELVSPFRVADRRCGLVLSRISGVL 140
QY 130 NNNQPMCSKLLTFLDKTSKLVQVEIPHNIATNATGMGELVSLVAQIAIDRNTVYIA 189
Db 141 EQTKIYAAQALLVYDLHNDLLRRHVLPAQOLKQGSIL-----LANLAVEDSDCENTPAYAA 196

QY	190	DEKGEGLIMYQNSDDSFHRLTSNTEDYDPRYTKLTVAGESFTVKNGICGIALS-PVTN--	246
Db	197	DLGSPGLVYVSWKDEBSRWQHFFHPDPMAGNFSINGIEFQWDDGLYGLALSXPLETGY	256
QY	247	-NLYYPSLSHGLYYVDTEQFRNPQVEENNVOYE-----GSODILANTQSFQKVSXN-GV	299
Db	257	ATLYFHPCLSTTEFSVDTSILRNKTLATSPMIYREFKVLGSRG-PNTQAGAEFLDPDTGV	315
QY	300	LFLGLVNGSIACVNEHQVLORESFDVVAQNEETLQMIWVKMKNLQPSGRINDEPNE	359
Db	316	LFLVALPMLNEVACWRTATDFSHSSQSRHNNNDTLVPPSDIKV-----DDQK	362
QY	360	YMLALSNRQMOKIINNDFNVDNFRILGANVDDLNRNTRCGRYHQNAGNQADNADN	419
Db	363	RLWVLSNQLPFFVYDELYAGSINFRILTASVKEAIENTAC---EIRTSPLDPVINKLGI	419
QY	420	QNANNONADNQNANKON	436
Db	420	LNTRIKLKSNSASSLRN	436
RESULT 4			
US-11-097-143-20991			
; Sequence 20991, Application US/11097143			
; Publication No. US20050208558A1			
; GENERAL INFORMATION:			
; APPLICANT: Venter, J. Craig			
; APPLICANT: et al.			
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID			
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE			
; FILE OF INVENTION: DROSOPHILA GENES.			
; FILE REFERENCE: CL000728			
; CURRENT FILING DATE: 2005-04-04			
; PRIOR APPLICATION NUMBER: US/11/097,143			
; PRIOR FILING DATE: 1999-10-05			
; PRIOR FILING DATE: 1999-10-19			
; PRIOR FILING DATE: 1999-10-28			
; PRIOR FILING DATE: 1999-10-28			
; PRIOR FILING DATE: 1999-11-12			
; PRIOR FILING DATE: 1999-12-28			
; PRIOR FILING DATE: 2000-01-12			
; PRIOR FILING DATE: 2000-02-24			
; PRIOR FILING DATE: 2000-03-23			
; NUMBER OF SEQ ID NOS: 43008			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 20991			
; LENGTH: 412			
; TYPE: PRT			
; ORGANISM: DROSOPHILA			
US-11-097-143-20991			
Query Match 14.9%; Score 415.5; DB 6; Length 412;			
Best Local Similarity 28.7%; Pred. No. 1.9e-25;			
Matches 117; Conservative 80; Mismatches 174; Indels 37; Gaps 14;			
QY	14	AHSMKVIYEWKHIDFDGSDERRDAAIKSGFDTKXNYPFDVD---RWRDXT---FVTIE	67
Db	19	AQALSVFGAYNLEFFSPQERQALRDGLYDPSVIPIDVDVYKHGDATPSIFVTIP	78
QY	68	R-NNGVPSLVNVTNKKGGKGLLRYP- -DWSFAKYEDCSGIVSAFKIADVDFRLWL	124
Db	79	RFAKGVPSLAYVTNEMRPNGLTQAYPSYEWKSHGADCNGLTSVYRTQIDECRMWIL	138
QY	125	DSGLVNNQPMCSPKLLTFDLKTSKLVKQVEIPHNIATNATGMGELVSLVAQAIDRNT	184
US-11-097-143-20973			
; Sequence 20973, Application US/11097143			
; Publication No. US20050208558A1			
; GENERAL INFORMATION:			
; APPLICANT: Venter, J. Craig			
; APPLICANT: et al.			
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID			
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE			
; FILE OF INVENTION: DROSOPHILA GENES.			
; FILE REFERENCE: CL000728			
; CURRENT FILING DATE: 2005-04-04			
; PRIOR APPLICATION NUMBER: US/11/097,143			
; PRIOR FILING DATE: 1999-10-05			
; PRIOR FILING DATE: 1999-10-19			
; PRIOR FILING DATE: 1999-10-28			
; PRIOR FILING DATE: 1999-10-28			
; PRIOR FILING DATE: 1999-11-12			
; PRIOR FILING DATE: 1999-12-28			
; PRIOR FILING DATE: 2000-01-12			
; PRIOR FILING DATE: 2000-02-24			
; PRIOR FILING DATE: 2000-03-23			
; NUMBER OF SEQ ID NOS: 43008			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 20973			
; LENGTH: 415			
; TYPE: PRT			
; ORGANISM: DROSOPHILA			
US-11-097-143-20973			
Query Match 14.6%; Score 408.5; DB 6; Length 415;			
Best Local Similarity 27.7%; Pred. No. 7.4e-25;			
Matches 114; Conservative 67; Mismatches 153; Indels 77; Gaps 12;			
QY	16	SMKVIYEWKHIDFDGSDERRDAAIKSGFDTKXNYPFDVD---RWRDXTFVTIER-N	69
Db	30	TVEILTQWGLEFGFPPTAQDRENAQAAGNLVPENGTPIDVQPMYANGQIRLFTTIPRFV	89
QY	70	NGVPSSLNVVTNKKGGKGLLRYPD- -WSPAKYEDCSGIVSAFKIADVDFRLWLDSG	127
Db	90	TGIPYTLATVSATQCRNGPLIQPYPNYSWHNANGDCDRITSAPRAVITECNQMWIDSG	149
QY	128	LNNQPMCSPKLLTFDLKTSKLVKQVEIPH-----NIAVNATGMGELVSL	174
Db	150	VIGTQ-LCCPQLQFALATDRLLHFRFPNDTYIPGSLFITPNVLVDPPPRCTC---	205
QY	175	AVQAIDRNTNMTVIAD- -KGEGLIMYQNSDDSFHRLTSNTFDYDPRYTKLTVAGESFTV	232

Qy 234 NGICGIALSPV-----TNNLYSPSSHGLYYVDTEQPRNPQYBENNVOYEGSOD--ILLNT 287
Db 267 DGIFSATLSGYKPDGSRDVFPHMASTNEFVSN---RVLQQEFNAARSDHGDDFHLIGT 323
Qy 288 Q-----SFGKWSKNGVLFLGLVNGSGIACVNEHQVLORESFDVVAQNEBETLQMIYSMK 341
Db 324 RGPSTQSTMKYDPRGTGVIFFAEVQKSGVGWCWTKSPFSTENHGSVYSNSS----- 374
Qy 342 IMENLPOSGRINDPEGNEYMLALSNRMOKIINDFNFDNVNFRILGANVDDLMRNTRC 399
Db 375 --EMVPSDLTIDBEG--YIWMNSNMPFIYVSKLDVEKYNFRIWROSTLLAKRGTV 428

RESULT 8
US-11-097-143-25236
; Sequence 25236, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25236
; LENGTH: 409
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-25236

Query Match 11.4%; Score 319.5; DB 6; Length 409;
Best Local Similarity 27.3%; Pred. No. 1.5e-17;
Matches 112; Conservative 70; Mismatches 167; Indels 61; Gaps 18;
Qy 17 MKVIEYKHXIDPFGSDERRDAAIKSGDFHTKQYPPDV-----DRWRDKTFVTIER-NN 70
Db 22 LHTLHQWNTLSIG-----DLSKGNRF-----LPVDVDIEYGDGHRHRTFLTPRLGM 69
Qy 71 GVPSSLNVVTKKKG--GGPLLRPVP--DWSFAKYDCSGIVSAFKIAVDKFDRLWLVDLS 126
Db 70 ATPFTLATVIAHNELVENPLRLEYPNEWHVPP--NNGSGITSARTYIDSCRWLVVDS 128
Qy 127 GLVNNQPMCSPKLITFDLTKSLKVOVEIPHNIAVNATTGMSGLVSAVOAIR-----181
Db 129 GQVNSLQ--LCPPQILTFDLVKDELQVRHALPPDSYI---PSVSIPTALVVDLAERGTPNR 184
Qy 182 -TNTMVIYADEKGLIMYQNSDDSFHRLTNTFDYDPRYKLTIVAGESFTVKNGICGIA 240
Db 185 CVGGRAYIADAGWGLIVFDSILTGRSMRIEHSMKPSP-----LLRLGRSSNSOAGIFTVS 240
Qy 241 LSP---VTNNLYSPSSHG-----LYYVDTEQF--RNQYBENNVOYEGSODILNTQSGF 291

Db 241 LSPSEVEDRFLYFHTLNSFNEMRVPVLSLINNETFWKSANASRDSFHSGLGTRGI---QCES 297
Qy 292 KVVSKNGVLFLGLVNGSGIACVNEHQVLORESFD--VVAQNEETLQMIYSMKIMENLPQS 349
Db 298 EVMQSQNLVCSLI--SIGALVKEESVSNVTADDLRVAVNPHKIKFVTGLKINRN----- 352
Qy 350 GRINDPEGNEYMLALSNRMOKIINDFNFDNVNFRILGANVDDLMRNTRC 399
Db 353 -----SKGBEELWALSQPKLFVGGDLPAVEVKFQIIGCRTADILLANTPC 397

RESULT 9
US-11-097-143-41712
; Sequence 41712, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41712
; LENGTH: 379
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-41712

Query Match 10.8%; Score 302.5; DB 6; Length 379;
Best Local Similarity 24.7%; Pred. No. 3.3e-16;
Matches 95; Conservative 70; Mismatches 181; Indels 39; Gaps 11;
Qy 35 RRDAAIKSGFDPHTKQYPPFDVDRWRDKTFVTIERNN--GVPSLLNVV--TNKKGKGGPLL 91
Db 13 RADSDPDNASYIPYNNVPMGATHEFRGLFVTMPRRRVGIPSTLNYIDLAEDGSNRSPKL 72
Qy 92 PYPDWSFAKYE--DCSGIVSAFKIAVDKFDRLWLVDLSGLV---NNQPMCSPKLITFDLKT 147
Db 73 AYPFALNQNASAEVLVSVRTSDACQRLWFDITGMLFYPNRRQIRRSIWWVDLAT 132
Qy 148 SKLVQKVEIPHNIAVNATTGMS--ELVSLAVOAIDRTNTMVIYADEKGLIMYQNSDDSF 206
Db 133 DOVLKRPDVPESI---AETGRGLASITVDVKAGCGGDAYAYIPDLVYRRLVYVYHLNRDRI 189
Qy 207 HRLTNTFDYDPRYKLTIVAGESFTVKNGICGIALSPV-----TNNLYSPSSHGLYYVD 262
Db 190 WSEFHNFNFDPLSGDLISGGQTERWDDGIFSIITLGAOKLDGSRDAYFHPMASTNEFVVS 249
Qy 263 TEQFRNQYBENNVOYEGSODILNTQSGKVVSK-----NGVLFGLVNGSGIACVN 314
Db 250 N---RVLQQESNAARSODHGNDFRVLGRSGPSTQSTMHAYDPTGVIFDETORNGVGCKW 306
Qy 315 EHQVLORESFDVVAQNEETLQMIYSMKIMENLPQSGRINDPEGNEYMLALSNRMOKIINN 374

[illegible]

Result No.	Score			Match	Query	ID		Description
	Score	Length	DB					
1	247	8.8	568	11	US-11-049-348-5	Sequence 5, Appl		
2	246.5	8.8	388	9	US-10-527-500-51	Sequence 51, Appl		
3	244.5	8.7	397	9	US-10-533-811-29	Sequence 29, Appl		
4	226.5	8.1	611	11	US-11-049-348-4	Sequence 4, Appl		
5	225.5	8.1	388	9	US-10-527-500-5	Sequence 5, Appl		
6	224.5	8.0	1046	11	US-11-165-819-6	Sequence 6, Appl		
7	224.5	8.0	1046	11	US-11-165-819-26	Sequence 26, Appl		
8	206.5	7.4	964	11	US-11-089-551A-30	Sequence 30, Appl		
9	205	7.3	393	9	US-10-527-500-7	Sequence 7, Appl		
10	204.5	7.3	412	9	US-10-533-811-23	Sequence 23, Appl		
11	204	7.3	700	11	US-11-096-568A-30799	Sequence 30799, A		
12	198	7.1	710	11	US-11-089-551A-33	Sequence 33, Appl		
13	197.5	7.1	399	9	US-10-533-811-63	Sequence 63, Appl		
14	193.5	6.9	477	11	US-11-089-551A-34	Sequence 34, Appl		
15	191.5	6.8	393	9	US-10-527-500-49	Sequence 49, Appl		
16	180	6.4	750	11	US-11-089-551A-32	Sequence 32, Appl		
17	178.5	6.4	454	11	US-11-089-551A-35	Sequence 35, Appl		
18	178	6.4	1075	11	US-11-089-551A-23	Sequence 23, Appl		
19	167.5	6.0	472	9	US-10-793-626-1902	Sequence 1902, Ap		
20	163.5	5.8	133	9	US-10-793-626-1924	Sequence 1924, Ap		
21	157.5	5.6	147	11	US-11-049-348-6	Sequence 6, Appl		

Db 251 GN-----NGNNDNNGNNGNT

QY
:
:
:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.


```

; APPLICANT: LI, Hung
; APPLICANT: HSIEH-LI, Hsui Mei
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEARL
; TITLE OF INVENTION: OYSTER CULTIVATION
; FILE REFERENCE: 505492000101
; CURRENT APPLICATION NUMBER: US/11/049,348
; CURRENT FILING DATE: 2005-02-01
; PRIOR APPLICATION NUMBER: US 10/086,510
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/310,070
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 611
; TYPE: PRT
; ORGANISM: Pinctada margaritifera
US-11-049-348-4

Query Match      8.1%; Score 226.5; DB 11; Length 611;
Best Local Similarity 36.8%; Pred. No. 3.7e-09;
Matches 60; Conservative 5; Mismatches 71; Indels 27; Gaps 6;

Qy 373 NNDNFNVDNFRILGANVDDLRRTRCGRYHQNQAGNADNQADNQANNQADNQNA 432
Db 300 NNGYNGNN-----GDNNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGN- 352
Qy 433 NKQNGNQNDNRQNDNQKQ-----GNRQNDNQKQNGR-QNDNQKQNGRQNGNQK 481
Db 353 NGNNGNGNGNGNDNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGN 412
Qy 482 D--NKQNGNQNDNQKNG-----NRQNDNQNDNQNDNQND 515
Db 413 NGNGNGNGNGNGNGNGNGNGDYGSNGNGNGNGNGNGNGNGNGNGNGN 455

RESULT 5
US-10-527-500-5
; Sequence 5, Application US/10527500
; Publication No. US20060004186A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; APPLICANT: Kamhawi, Shaden
; APPLICANT: Belkaid, Yasmine
; APPLICANT: Fischer, Laurent Bernard
; APPLICANT: Audonnet, Jean-Cristophe
; APPLICANT: Milward, Francis William
; TITLE OF INVENTION: P. ARIASI POLYPEPTIDES AND P. PERNICIOSUS POLYPEPTIDES AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 4239-66903-02
; CURRENT APPLICATION NUMBER: US/10/527,500
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/US2003/029833
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 60/425,852
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/412,327
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Phlebotomus ariasi
US-10-527-500-5

Query Match      8.1%; Score 225.5; DB 9; Length 388;
Best Local Similarity 22.7%; Pred. No. 2.4e-09;
Matches 99; Conservative 66; Mismatches 174; Indels 97; Gaps 16;

; APPLICANT: Ma, Hui
; APPLICANT: Dillin, Andrew
; APPLICANT: Hunter, Tony
; TITLE OF INVENTION: Increasing Life Span by Modulation of
; TITLE OF INVENTION: the Smek Gene
; FILE REFERENCE: 532792001900
; CURRENT APPLICATION NUMBER: US/11/165,819
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 60/583,284
; PRIOR FILING DATE: 2004-06-25
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1046
; TYPE: PRT
; ORGANISM: Dictyostelium discoideum
US-11-165-819-6

Query Match      8.0%; Score 224.5; DB 11; Length 1046;
Best Local Similarity 19.4%; Pred. No. 1.1e-08;
Matches 80; Conservative 49; Mismatches 105; Indels 179; Gaps 13;

Qy 261 VDTQFRNPQYENNVQYEGSQDILNTQSFQKVVSKNGVFLGLVGNAGIACVNEHVLQ 320
Db 621 IKOSSPESPETSCNN-----NDSNDIDSK-----PIGNKKN--HNYQRTQ 662
Qy 321 RE-----SPDVVAQNEETLQIMIVSMKIMENLPQSGRINDPQEGNMYLALS--NRM 368
Db 663 REIDEEEEEAYFNRDDSDSDSDDEDELIPISINN-----NNNNNNKQICTNNENN 715
Qy 369 QKIINNDNFNVDNFRILGAN-----VDDL-----RN 396
Db 716 EK---NDDNTEKNDNTNNGNGSSHIKIVDYEDDEDEDEDEINKSVESDDIVKHEI 772
```


Dd 58 SSDSGSPSPGQNNN-----DGNNGNNNDNNNNNGNNNDN-NGGWK-DNNN 106

Qy 471 NGNRQNGKNQDNKGQRNQDKENGRRQNDDNN-QNDNNRN 513
||| ||| ||| ||| :||| |||
Db 107 NGNNNGNNGGNDNGNNNGN---NNDNNQQNGGSNNRS 146

RESULT 12

US-11-089-551A-33
; Sequence 33, Application US/11089551A
; Publication No. US20050266242A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al.
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40025A
; CURRENT APPLICATION NUMBER: US/11/089,551A
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US 60/559,286
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-11-089-551A-33

Query Match 7.1%; Score 198; DB 11; Length 710;
Best Local Similarity 20.7%; Pred.No.6.le-07;
Matches 110; Conservative 63; Mismatches 192; Indels 166; Gaps 24;

Qy 25 HIDFGSDERRDAAIKGSEFDHTKNYPDFVDWRWDKTFTTERNGVPSLLNVVTNKKG 84
:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db 309 HSSNNYSSDSKDHT--SKYDHNFH-----AKNGKV-SDTNYGHNSKV 349

Qy 85 KGGPLLRPPDPWSFAKYDCSIVSAFKIADVDFRLWVLDSLGLVNNOQMCPCKLITPD 144
:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db 350 K-----RKOTDAKRKRKDSNSTWA-----VMDSRDYGNTVKNSSR----D 386

Qy 145 LKTSKL VKQEIPHN-----TAVNATTCGMGELVSLAQVIDRTHMTVIADKEGRG 195
:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db 387 MRKC NKYTSMGVHKRGTVWC/KQMANTRNVTSGSYDYC-----TNDRGTV---GKG 433

Qy 196 LIMYQNSDDSFRHLTSNTFYDPRYTKLTVAAGESPTVKNGIGICIALSPVTNNLYISPLSS 255
434 W-----NSSVS HWTVRYG-----SPA VPACADSTCTTSVYA-TDT 469

Qy 256 HGYYVYDTQEPNPQYEENVO--YEGODILNTQSFGKWVGKGVLFGLGVNSGIACV 313
:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db 470 NGTKW-DTCTKNCKDVKNVKCKCHKGS-----TVKNRGGASK 506

Qy 314 NEH-----QVLQRESF--DVDQAONEETLOM--IVSMKI MENLPQSGRINDP 355
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Db 507 NKHADGSSDSGDNGYGYTYKVTSRDNSVRDATKENSNNSRVGSSAGSKSKXNHKKHGHSRA 566

Qy 356 EQNEY--MLALSNRMOKIIINDFENDVFNRI LGANVDLDLMETRCCR YHH -QNAGNQNA 412
:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db 567 RGVSVSSVRKSNSRNSRVNMNAGTA N-----NAMSNSYN NVYSGNNN 610

Qy 413 DNQONADNQ--ANNQONADNQANKGNR QDNRRQNDKNQGNRRQNDKNQGNRRQNDKQ 470
:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
Db 611 GNSNGD NSDRANGTNSYN-NVYSNNNN NYNNSGYSSMMNSRSVSHNNNNNTNYNNND --- 666

Qy 471 NGNRQNGKNQDNKGQRNQDKENGRRQNDDNN-QNDNNRN 521
||| ||| ||| ||| :||| |||
Db 667 -----NDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNDT SYRYS 707

RESULT 13

US-10-533-811-63
; Sequence 63, Application US/10533811
; Publication No. US20060051364A1
; GENERAL INFORMATION:

Query Match		6.9%; Score 193.5; DB 11; Length 477;
Best Local Similarity		23.4%; Pred. No. 7.8e-07;
Matches		65; Conservative 37; Mismatches 121; Indels 55; Gaps 10;
Qy	267	RNPOYENNQYEGSQDILANTQSGKVVSKNGVLFLGLVG--NSGIACVNEHQVLQRESF 324
Db	40	RSQYKDKNA---GSN--ANATSSG---STDSAVTDGTSGARNSSSKKKKHDTMGHSSS 91
Qy	325	DVVAQNBEETLQMIYMKIMENLPQSGRINDEPEGNEYMLALSNRMQKIINNDNF- 378
Db	92	DTSSSN-----RSNKYTGVKKTSVKKRSNHNVSYSYVKDK 126
Qy	379	-----NDVNFRLGANVDLMBN--TRCGRYHQNAGNQADNQADNQANNNQADNQ 430
Db	127	NCVTKASKDVRSAVMGNTTGNVKNSTTTGNGNNKNSNSTVTSTNNNSANNAAGSNT 186
Qy	431	NANKONGNRQDN---RQNDKQNGNRQNDKQNGNRQNDKQNGNRQNGKQNDKQNDKQND 486
Db	187	SANK-NYYKNDSSGYTAASTTMTYTNSD--TNATGMNTHVNNNNNNNSNNSNNSN 244
Qy	487	GNRQDNKRGNRQNDQNDQNDQNDQNDQNDQNDQNDQNDQNDQNDQNDQNDQNDQNDQND 524
Db	245	NN 282

Search completed: May 3, 2006, 19:18:53
Job time : 33.1893 secs

RESULT 15									
US-10-527-500-49									
; Sequence 49, Application US/10527500									
; Publication No. US20060004186A1									
; GENERAL INFORMATION:									
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS									
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND									
; APPLICANT: HUMAN SERVICES									
; APPLICANT: Valenzuela, Jesus G.									
; APPLICANT: Ribeiro, Jose M.C.									
; APPLICANT: Kanhawi, Shaden									
; APPLICANT: Belkaid, Yasmine									
; APPLICANT: Fischer, Laurent Bernard									
; APPLICANT: Audonnet, Jean-Cristophe									
; APPLICANT: Milward, Francis William									
; TITLE OF INVENTION: P. ARIASI POLYPEPTIDES AND P. PERNICIOSUS POLYPEPTIDES AND									
; TITLE OF INVENTION: METHODS OF USE									
; FILE REFERENCE: 4239-66903-02									
; CURRENT APPLICATION NUMBER: US/10/527,500									
; CURRENT FILING DATE: 2005-03-11									
; PRIOR APPLICATION NUMBER: PCT/US2003/029833									
; PRIOR FILING DATE: 2003-09-18									
; PRIOR APPLICATION NUMBER: US 60/425,852									
; PRIOR FILING DATE: 2002-11-12									
; PRIOR APPLICATION NUMBER: US 60/412,327									
; PRIOR FILING DATE: 2002-09-19									
; NUMBER OF SEQ ID NOS: 87									
; SOFTWARE: PatentIn version 3.2									
; SEQ ID NO 49									
; LENGTH: 393									
; TYPE: PRT									
; ORGANISM: Phlebotomus perniciosus									
US-10-527-500-49									
Query Match									
Best Local Similarity 6.8%; Score 191.5; DB 9; Length 393;									
Matches 91; Conservative 74; Mismatches 168; Indels 75; Gaps 20;									
Qy	21	YEWKHIDPFGSDE---RDAAIKSGEFDHTKNYPFDVDRWRDKTFVTIERNN-GVPSL 76							
Db	25	YAWKNISYE-GVDPALFNIDNIPTG-FVH-----DAINKKIFIAVPRSPQIPFTL 74							
Qy	77	NVVTNKKGKGLLRYPDWS--FAKYEDCSGIVSAFKIADVDFRLWLDSGLVN---- 130							
Db	75	TELDITK-----HPERSPPLSKFPGSKDLINVQVIDECRLMTADVGRVDYKGD 125							
Qy	131	NNQPMCSPKLLTFDLKTSKL--VKQVEIPHNIANNATGMGELVSLAVQAIDRTN---- 183							

Page Blank (up)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 18:53:48 ; Search time 175.483 Seconds
(without alignments)
1034.083 Million cell updates/sec

Title: US-10-525-567-4
Perfect score: 2178
Sequence: 1 NLRGSLNKLSPILHEWKF.....NTRCENPDNDTRPFKISHL 413

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq.21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2177	99.9	413	8 ADL27607	Adl27607 Honey bee
2	2177	99.9	414	8 ADL27617	Adl27617 Honey bee
3	2177	99.9	432	4 AAG78710	Aag78710 Oxygen pr
4	2177	99.9	432	4 AAG78815	Aag78815 Bee prote
5	2177	99.9	432	8 ADL27619	Adl27619 Honey bee
6	1415.5	65.0	524	8 ADL27606	Adl27606 Honey bee
7	1415.5	65.0	544	8 ADL27616	Adl27616 Honey bee
8	1406.5	64.6	544	8 ADL27618	Adl27618 Honey bee
9	452.5	20.8	541	4 ABB60127	Abb60127 Drosophil
10	448	20.6	438	4 ABB60071	Abb60071 Drosophil
11	435.5	20.0	453	4 ABB71124	Abb71124 Drosophil
12	422	19.4	426	4 ABB66147	Abb66147 Drosophil
13	415	19.1	412	4 ABB64733	Abb64733 Drosophil
14	411.5	18.9	415	4 ABB64727	Abb64727 Drosophil
15	366	16.8	429	4 ABB67082	Abb67082 Drosophil
16	358	16.4	530	4 ABB71802	Abb71802 Drosophil
17	357	16.4	379	4 ABB71640	Abb71640 Drosophil
18	343.5	15.8	409	4 ABB66148	Abb66148 Drosophil
19	331.5	15.2	316	4 ABB58294	Abb58294 Drosophil
20	276.5	12.7	397	8 ADO43422	Ado43422 Lutzomyia
21	260	11.9	388	8 ADM16728	Adm16728 PERL-P6-H
22	258	11.8	393	4 ABB57969	Abb57969 Drosophil
23	256	11.8	388	8 ADM16682	Adm16682 PRL-P4-C1
24	240.5	11.0	393	8 ADM16684	Adm16684 PRL-P4-D6

25	233	10.7	382	4	ABB68627	Abb68627 Drosophil
26	229.5	10.5	412	8	ADO43416	Ado43416 Lutzomyia
27	229	10.5	394	6	ABR91192	AbR91192 P. papata
28	214	9.8	393	8	ADM16726	Adm16726 PERL-P7-G
29	209.5	9.6	400	6	ABR91193	AbR91193 P. papata
30	184	8.4	399	8	ADO43456	Ado43456 Lutzomyia
31	156	7.2	342	4	ABB63308	Abb63308 Drosophil
32	138	6.3	25	8	ADL27605	Adl27605 Honey bee
33	123	5.6	1100	2	AAR15783	Aar15783 B.thuring
34	122.5	5.6	575	8	ADS08188	AdS08188 Staphyloc
35	116	5.3	946	5	ABP74063	Abp74063 Candida a
36	114	5.2	414	5	ABB54432	Abb54432 Lactococc
37	113.5	5.2	1530	5	ABB47329	Abb47329 Listeria
38	111	5.1	4643	4	ABB71609	Abb71609 Drosophil
39	110	5.1	391	6	ABU43455	Abu43455 Protein e
40	110	5.1	742	4	ABR67313	AbR67313 Drosophil
41	110	5.1	742	8	ADQ89700	Adq89700 Antagonis
42	110	5.1	1088	4	ABR67108	AbR67108 Drosophil
43	110	5.1	1088	8	ADQ89698	Adq89698 Antagonis
44	109	5.0	4688	6	ABU48941	Abu48941 Protein e
45	108.5	5.0	1427	9	ABM91413	Abm91413 M. xanthu

ALIGNMENTS

RESULT 1

ADL27607
ID ADL27607 standard; protein; 413 AA.

XX ADL27607;

AC AC

DT 03-JUN-2004 (first entry)

XX Honey bee RJP55 mature protein, SEQ ID 4.

XX Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
XX royal jelly protein; allergy; pollinosis; atopic dermatitis;
XX contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP55.

OS Apis mellifera.

XX WO2004019971-A1.

XX 11-MAR-2004.

XX 26-AUG-2003; 2003WO-JP010795.

XX 29-AUG-2002; 2002JP-00252087.

XX 30-JAN-2003; 2003JP-00022776.

XX (HAYA/) HAYASHIBARA K.

XX Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;

XX WPI: 2004-248191/23.

XX N-PSDB; ADL27609.

XX Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,
XX atopic dermatitis, contact hypersensitivity, bronchial asthma and
XX allergic rhinitis, comprise protein originated from royal jelly.

XX Claim 2; SEQ ID NO 4; 78pp; Japanese.

XX The present invention relates to novel antiallergic agents, which
XX comprise as an active ingredient, peptides ADL27604 and ADL27605, which
XX are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606
XX and ADL27607). The agents can be used to relieve symptoms accompanying an
XX allergic disease e.g. pollinosis, atopic dermatitis, contact
XX hypersensitivity, bronchial asthma and allergic rhinitis, which are
XX applicable in foods, cosmetics and drugs.

XX Sequence 413 AA;

Query Match		99.9%;	Score 2177;	DB 8;	Length 413;
Best Local Similarity		100.0%;	Pred. No. 2.8e-193;		
Matches 413;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	NILRGESLNKSLPILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSDIDQWHDKIFVT	60		
Db	1	NILRGESLNKSLPILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSDIDQWHDKIFVT	60		
Qy	61	MLRYNGVPSSLNVISKVGCGPLLPQYPDWSFAKYDDCSGIVSASKLAIDKCDRLWVLD	120		
Db	61	MLRYNGVPSSLNVISKVGCGPLLPQYPDWSFAKYDDCSGIVSASKLAIDKCDRLWVLD	120		
Qy	121	SGLVNNTQPMCSKPLTFTDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNS	180		
Db	121	SGLVNNTQPMCSKPLTFTDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNS	180		
Qy	181	DTMVYIADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALS	240		
Db	181	DTMVYIADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALS	240		
Qy	241	PMTNNLYSPVASTSLYYNTEQFRTSDYQNDIHVEGVQNLDTQSSAKVSKSVGLFF	300		
Db	241	PMTNNLYSPVASTSLYYNTEQFRTSDYQNDIHVEGVQNLDTQSSAKVSKSVGLFF	300		
Qy	301	GLVGSALGCGWNEHRTLERHNIRTVAVQSDTLQMIASMKIKEAXPHVPIFDRYINREYIL	360		
Db	301	GLVGSALGCGWNEHRTLERHNIRTVAVQSDTLQMIASMKIKEAXPHVPIFDRYINREYIL	360		
Qy	361	VLSNKMOKMVNNDNFDDVFRIMNANVNELILNTRCENPDNDRTPPKISIH	413		
Db	361	VLSNKMOKMVNNDNFDDVFRIMNANVNELILNTRCENPDNDRTPPKISIH	413		
RESULT 2					
ID	ADL27617 standard; protein; 414 AA.				
XX					
AC	ADL27617;				
XX					
DT	03-JUN-2004 (first entry)				
XX					
DE	Honey bee RJP55.				
XX					
KW	Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;				
KW	royal jelly protein; allergy; pollinosis; atopic dermatitis;				
KW	contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP55.				
XX					
OS	Apis mellifera.				
XX					
PN	W02004019971-A1.				
XX					
PD	11-MAR-2004.				
XX					
PF	26-AUG-2003; 2003WO-JP010795.				
XX					
PR	29-AUG-2002; 2002JP-00252087.				
PR	30-JAN-2003; 2003JP-00022776.				
XX					
PA	(HAYA/) HAYASHIBARA K.				
XX					
PI	Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;				
XX					
DR	WPI; 2004-248191/23.				
DR	N-PSDB; ADL27609.				
XX					
PT	Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,				
PT	atopic dermatitis, contact hypersensitivity, bronchial asthma and				
PT	allergic rhinitis, comprise protein originated from royal jelly.				
XX					
PS	Disclosure; Page 62-65; 78pp; Japanese.				
XX					
CC	The present invention relates to novel antiallergic agents, which				

Query Match		99.9%;	Score 2177;	DB 8;	Length 414;
Best Local Similarity		99.8%;	Pred. No. 2.8e-193;		
Matches 412;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	NILRGESLNKSLPILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSDIDQWHDKIFVT	60		
Db	2	NILRGESLNKSLPILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSDIDQWHDKIFVT	61		
Qy	61	MLRYNGVPSSLNVISKVGCGPLLPQYPDWSFAKYDDCSGIVSASKLAIDKCDRLWVLD	120		
Db	62	MLRYNGVPSSLNVISKVGCGPLLPQYPDWSFAKYDDCSGIVSASKLAIDKCDRLWVLD	121		
Qy	121	SGLVNNTQPMCSKPLTFTDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNS	180		
Db	122	SGLVNNTQPMCSKPLTFTDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNS	181		
Qy	181	DTMVYIADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALS	240		
Db	182	DTMVYIADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALS	241		
Qy	241	PMTNNLYSPVASTSLYYNTEQFRTSDYQNDIHVEGVQNLDTQSSAKVSKSVGLFF	300		
Db	242	PMTNNLYSPVASTSLYYNTEQFRTSDYQNDIHVEGVQNLDTQSSAKVSKSVGLFF	301		
Qy	301	GLVGSALGCGWNEHRTLERHNIRTVAVQSDTLQMIASMKIKEAXPHVPIFDRYINREYIL	360		
Db	302	GLVGSALGCGWNEHRTLERHNIRTVAVQSDTLQMIASMKIKEALPHVPIFDRYINREYIL	361		
Qy	361	VLSNKMOKMVNNDNFDDVFRIMNANVNELILNTRCENPDNDRTPPKISIH	413		
Db	362	VLSNKMOKMVNNDNFDDVFRIMNANVNELILNTRCENPDNDRTPPKISIH	414		
RESULT 3					
AAG78710					
ID	AAG78710 standard; protein; 432 AA.				
XX					
AC	AAG78710;				
XX					
DT	11-DEC-2001 (first entry)				
XX					
DE	Oxygen promoter related protein.				
XX					
KW	Oxygen promoter; bee; royal jelly; cardiant; vulnerary;				
KW	cardiopulmonary function.				
XX					
OS	Apis mellifera.				
XX					
PN	JP2001172195-A.				
XX					
PD	26-JUN-2001.				
XX					
PF	15-DEC-1999; 99JP-00356005.				
XX					
PR	15-DEC-1999; 99JP-00356005.				
XX					
PA	(POKK) POLA CHEM IND INC.				
XX					
DR	WPI; 2001-592558/67.				
DR	N-PSDB; AAI64996.				
XX					
PT	Agent for promoting oxygen in cells to improve cardiopulmonary function,				
PT	comprises protein in royal jelly which comprises oxygen enhancing effect.				

CC	comprise as an active ingredient, peptides ADL27604 and ADL27605, which					
CC	are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606					
CC	and ADL27607). The agents can be used to relieve symptoms accompanying an					
CC	allergic disease e.g. pollinosis, atopic dermatitis, contact					
CC	hypersensitivity, bronchial asthma and allergic rhinitis, which are					
CC	applicable in foods, cosmetics and drugs. The present sequence is a honey					
CC	bee RJP.					
XX						
SQ	Sequence 414 AA;					
	Query Match	99.9%;	Score 2177;	DB 8;	Length 414;	
	Best Local Similarity	99.8%;	Pred. No. 2.8e-193;			
	Matches 412;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
Qy	1	NILRGESLNKSLPILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSDIDQWHDKIFVT	60			
Db	2	NILRGESLNKSLPILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSDIDQWHDKIFVT	61			
Qy	61	MLRYNGVPSSLNVISKVGCGPLLPYPDPWSFAKYDDCSGIVSASKLAIDKCDRLWVLD	120			
Db	62	MLRYNGVPSSLNVISKVGCGPLLPYPDPWSFAKYDDCSGIVSASKLAIDKCDRLWVLD	121			
Qy	121	SGLVNNTQPMCSKPLTFTDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNS	180			
Db	122	SGLVNNTQPMCSKPLTFTDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNS	181			
Qy	181	DTMVYIADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALS	240			
Db	182	DTMVYIADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALS	241			
Qy	241	PMTNNLYSPVASTSLYYNTEQFRTSDYQNDIHVEGVQNLDTQSSAKVSKSVGLFF	300			
Db	242	PMTNNLYSPVASTSLYYNTEQFRTSDYQNDIHVEGVQNLDTQSSAKVSKSVGLFF	301			
Qy	301	GLVGSALGCGWNEHRTLERHNIRTVAVQSDTLQMIASMKIKEAXPHVPIFDRYINREYIL	360			
Db	302	GLVGSALGCGWNEHRTLERHNIRTVAVQSDTLQMIASMKIKEALPHVPIFDRYINREYIL	361			
Qy	361	VLSNKMOKMVNNDNFDDVFRIMNANVNELILNTRCENPDNDRTPPKISIH	413			
Db	362	VLSNKMOKMVNNDNFDDVFRIMNANVNELILNTRCENPDNDRTPPKISIH	414			
RESULT 3						
AAG78710						
ID	AAG78710 standard; protein; 432 AA.					
XX						
AC	AAG78710;					
XX						
DT	11-DEC-2001 (first entry)					
XX						
DE	Oxygen promoter related protein.					
XX						
KW	Oxygen promoter; bee; royal jelly; cardiant; vulnerary;					
KW	cardiopulmonary function.					
XX						
OS	Apis mellifera.					
XX						
PN	JP2001172195-A.					
XX						
PD	26-JUN-2001.					
XX						
PF	15-DEC-1999; 99JP-00356005.					
XX						
PR	15-DEC-1999; 99JP-00356005.					
XX						
PA	(POKK) POLA CHEM IND INC.					
XX						
DR	WPI; 2001-592558/67.					
DR	N-PSDB; AAI64996.					
XX						
PT	Agent for promoting oxygen in cells to improve cardiopulmonary function,					
PT	comprises protein in royal jelly which comprises oxygen enhancing effect.					

XX PS Disclosure; Page 9-10; 10pp; Japanese.
 XX PA
 XX XX
 CC The present invention relates to an agent for promoting oxygen,
 CC comprising a protein in royal jelly which has an oxygen enhancing effect.
 CC This can be used to promote oxygen in cells, causing an improvement in
 CC pulmonary function. The present sequence is a protein which can be used
 CC in the agent of the invention
 XX XX
 SQ Sequence 432 AA;
 Query Match 99.9%; Score 2177; DB 4; Length 432;
 Best Local Similarity 100.0%; Pred. No. 3e-193;
 Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NILRGESLNKSLPILHEWKPFDDYFGSDERRQDAILSGEYDYKKNYPSDIDQWHDKIFVT 60
 Db 20 NILRGESLNKSLPILHEWKPFDDYFGSDERRQDAILSGEYDYKKNYPSDIDQWHDKIFVT 79
 Qy 61 MLRYNGVPSSLNVISKVGDPGLLPYPDWSFAKYDDCGIVSASKLAIDKCDRLWVLD 120
 Db 80 MLRYNGVPSSLNVISKVGDPGLLPYPDWSFAKYDDCGIVSASKLAIDKCDRLWVLD 139
 Qy 121 SGLVNNTQPMCSPKLLTFDLTTSQLLKQVEIPHDAVNATTKGRLSSLAQSILDCNTNS 180
 Db 140 SGLVNNTQPMCSPKLLTFDLTTSQLLKQVEIPHDAVNATTKGRLSSLAQSILDCNTNS 199
 Qy 181 DTWYIADKEGELIVYHNSDDSFHRLTNTFDYDPKFTKMTIDGESYTAQDGISGMALS 240
 Db 200 DTWYIADKEGELIVYHNSDDSFHRLTNTFDYDPKFTKMTIDGESYTAQDGISGMALS 259
 Qy 241 PMTNLYSPVASTSLYYVNTQEQRTSDYQNDIHVEGVQNLDTQSSAKVSKGVLF 300
 Db 260 PMTNLYSPVASTSLYYVNTQEQRTSDYQNDIHVEGVQNLDTQSSAKVSKGVLF 319
 Qy 301 GLVGSALGCWNEHRTLERHNIRTVQSDTELQMIASMKIEXAPHVPIDFRIYINREYIL 360
 Db 320 GLVGSALGCWNEHRTLERHNIRTVQSDTELQMIASMKIEXAPHVPIDFRIYINREYIL 379
 Qy 361 VLSNKMQRWVNDNFDDVFNFRIMNANVNELILNTRCENPDNDRTPPKISIH 413
 Db 380 VLSNKMQRWVNDNFDDVFNFRIMNANVNELILNTRCENPDNDRTPPKISIH 432
 RESULT 4
 AAG78815
 ID AAG78815 standard; protein; 432 AA.
 XX AC AAG78815;
 XX XX
 DT 27-NOV-2001 (first entry)
 XX DE
 XX DE Bee protein.
 XX KW Bee; lactic acid accumulation inhibitor; royal jelly; muscular fatigue.
 XX OS
 XX APIS mellifera.
 XX XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Signal_peptide
 FT Protein 20..432
 FT /label= Mature_bee_protein
 FT Misc-difference 363
 FT /label= unknown
 FT /note= "Encoded by CTW, given as Xaa in specification"
 XX JP2001172190-A.
 XX PN
 XX PD 26-JUN-2001.
 XX XX
 PF 15-DEC-1999; 99JP-00356006.
 XX XX

PR 15-DEC-1999; 99JP-00356006.
 XX (POKK) POLA CHEM IND INC.
 XX PA
 XX XX
 DR WPI; 2001-592556/67.
 DR N-PSDB; AAI65041.
 XX XX
 PT Lactic acid accumulation inhibitor comprises protein contained in royal
 PT jelly, useful for restoration, improvement and release of muscular
 PT fatigue.
 XX XX
 PS Disclosure; Page 9-10; 10pp; Japanese.
 XX PA
 XX XX
 CC The present invention relates to a lactic acid accumulation inhibitor.
 CC The inhibitor comprises a protein contained in royal jelly having lactic
 CC acid accumulation inhibiting activity as the active component. The lactic
 CC acid accumulation inhibitor is used for restoration, improvement and
 CC release of muscular fatigue. The present sequence is a bee protein, which
 CC was used in the present invention
 XX XX
 SQ Sequence 432 AA;
 Query Match 99.9%; Score 2177; DB 4; Length 432;
 Best Local Similarity 100.0%; Pred. No. 3e-193;
 Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NILRGESLNKSLPILHEWKPFDDYFGSDERRQDAILSGEYDYKKNYPSDIDQWHDKIFVT 60
 Db 20 NILRGESLNKSLPILHEWKPFDDYFGSDERRQDAILSGEYDYKKNYPSDIDQWHDKIFVT 79
 Qy 61 MLRYNGVPSSLNVISKVGDPGLLPYPDWSFAKYDDCGIVSASKLAIDKCDRLWVLD 120
 Db 80 MLRYNGVPSSLNVISKVGDPGLLPYPDWSFAKYDDCGIVSASKLAIDKCDRLWVLD 139
 Qy 121 SGLVNNTQPMCSPKLLTFDLTTSQLLKQVEIPHDAVNATTKGRLSSLAQSILDCNTNS 180
 Db 140 SGLVNNTQPMCSPKLLTFDLTTSQLLKQVEIPHDAVNATTKGRLSSLAQSILDCNTNS 199
 Qy 181 DTWYIADKEGELIVYHNSDDSFHRLTNTFDYDPKFTKMTIDGESYTAQDGISGMALS 240
 Db 200 DTWYIADKEGELIVYHNSDDSFHRLTNTFDYDPKFTKMTIDGESYTAQDGISGMALS 259
 Qy 241 PMTNLYSPVASTSLYYVNTQEQRTSDYQNDIHVEGVQNLDTQSSAKVSKGVLF 300
 Db 260 PMTNLYSPVASTSLYYVNTQEQRTSDYQNDIHVEGVQNLDTQSSAKVSKGVLF 319
 Qy 301 GLVGSALGCWNEHRTLERHNIRTVQSDTELQMIASMKIEXAPHVPIDFRIYINREYIL 360
 Db 320 GLVGSALGCWNEHRTLERHNIRTVQSDTELQMIASMKIEXAPHVPIDFRIYINREYIL 379
 Qy 361 VLSNKMQRWVNDNFDDVFNFRIMNANVNELILNTRCENPDNDRTPPKISIH 413
 Db 380 VLSNKMQRWVNDNFDDVFNFRIMNANVNELILNTRCENPDNDRTPPKISIH 432
 RESULT 5
 ADL27619
 ID ADL27619 standard; protein; 432 AA.
 XX AC ADL27619;
 XX XX
 DT 03-JUN-2004 (first entry)
 XX DE
 XX DE Honey bee MRJP1.
 XX KW Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
 KW royal jelly protein; allergy; pollinosis; atopic dermatitis;
 KW contact hypersensitivity; bronchial asthma; allergic rhinitis; MRJP1.
 XX OS
 XX APIS mellifera.
 XX XX
 FH Key Location/Qualifiers
 FT Peptide 1..19

```
FT Protein /label= Signal_peptide
FT 20..432
FT /label= Mature_protein
XX WO2004019971-A1.
XX 11-MAR-2004.
XX
XX 26-AUG-2003; 2003WO-JP010795.
XX
XX 29-AUG-2002; 2002JP-00252087.
XX 30-JAN-2003; 2003JP-00022776.
XX (HAYA/) HAYASHIBARA K.
XX
XX Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;
XX
XX WPI; 2004-248191/23.
XX N-PSDB; ADL27606.
XX
XX Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,
XX atopic dermatitis, contact hypersensitivity, bronchial asthma and
XX allergic rhinitis, comprise protein originated from royal jelly.
XX
XX Disclosure; Page 70-72; 78pp; Japanese.
XX
XX The present invention relates to novel antiallergic agents, which
XX comprise as an active ingredient, peptides ADL27604 and ADL27605, which
XX are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606
XX and ADL27607). The agents can be used to relieve symptoms accompanying an
XX allergic disease e.g. pollinosis, atopic dermatitis, contact
XX hypersensitivity, bronchial asthma and allergic rhinitis, which are
XX applicable in foods, cosmetics and drugs. The present sequence is a honey
XX bee major RJP.
XX
XX Sequence 432 AA;
XX
XX Query Match 99.9%; Score 2177; DB 8; Length 432;
XX Best Local Similarity 100.0%; Pred. No. 3e-193;
XX Matches 413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 NILRGESLNKSLPTLHEWKFFDYDFGSDERRQDAILSGEYDYKKNYPSDIDQWHDKIFVT 60
Db 20 NILRGESLNKSLPTLHEWKFFDYDFGSDERRQDAILSGEYDYKKNYPSDIDQWHDKIFVT 79
XX
Qy 61 MLRNGVPSSLNVLISKVGDGGLLPQYPDWSFAKYDDCSGIVSASKLAIDKCDRLWVLD 120
Db 80 MLRNGVPSSLNVLISKVGDGGLLPQYPDWSFAKYDDCSGIVSASKLAIDKCDRLWVLD 139
XX
Qy 121 SGLVNNTPQMCSPKLLTFDLTTSQLLKQVEIPHDAVNATTGKRLSSLAVQSLDCNTNS 180
Db 140 SGLVNNTPQMCSPKLLTFDLTTSQLLKQVEIPHDAVNATTGKRLSSLAVQSLDCNTNS 199
XX
Qy 181 DTWVYIADEKGEGLIVHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGNALS 240
Db 200 DTWVYIADEKGEGLIVHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGNALS 259
XX
Qy 241 PMTNNLVYSPVASTSLVYVNTQERTSDYQONDHYEGVQNLDTQSSAKVSKSVGLFF 300
Db 260 PMTNNLVYSPVASTSLVYVNTQERTSDYQONDHYEGVQNLDTQSSAKVSKSVGLFF 319
XX
Qy 301 GLVGDSALGCWNEHRTLERNIRTVASDETLQMIASMKIKEAXPHVPIFDRIYNREYIL 360
Db 320 GLVGDSALGCWNEHRTLERNIRTVASDETLQMIASMKIKEAXPHVPIFDRIYNREYIL 379
XX
Qy 361 VLSNMQKMNNDNFDDVFNFRIMNANVNLILNTRCENPDNDRTPEKISHL 413
Db 380 VLSNMQKMNNDNFDDVFNFRIMNANVNLILNTRCENPDNDRTPEKISHL 432
XX
XX RESULT 6
XX ADL27606
XX ID ADL27606 standard; protein; 524 AA.
```

```
XX AC ADL27606;
XX 03-JUN-2004 (first entry)
XX Honey bee RJP70 mature protein, SEQ ID 3.
XX
XX Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;
XX royal jelly protein; allergy; pollinosis; atopic dermatitis;
XX contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP70.
XX
XX Apis mellifera.
XX
XX WO2004019971-A1.
XX 11-MAR-2004.
XX
XX 26-AUG-2003; 2003WO-JP010795.
XX
XX 29-AUG-2002; 2002JP-00252087.
XX 30-JAN-2003; 2003JP-00022776.
XX (HAYA/) HAYASHIBARA K.
XX
XX Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;
XX
XX WPI; 2004-248191/23.
XX N-PSDB; ADL27608.
XX
XX Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,
XX atopic dermatitis, contact hypersensitivity, bronchial asthma and
XX allergic rhinitis, comprise protein originated from royal jelly.
XX
XX Claim 1; SEQ ID NO 3; 78pp; Japanese.
XX
XX The present invention relates to novel antiallergic agents, which
XX comprise as an active ingredient, peptides ADL27604 and ADL27605, which
XX are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606
XX and ADL27607). The agents can be used to relieve symptoms accompanying an
XX allergic disease e.g. pollinosis, atopic dermatitis, contact
XX hypersensitivity, bronchial asthma and allergic rhinitis, which are
XX applicable in foods, cosmetics and drugs.
XX
XX Sequence 524 AA;
XX
XX Query Match 65.0%; Score 1415.5; DB 8; Length 524;
XX Best Local Similarity 65.0%; Pred. No. 2.9e-122;
XX Matches 264; Conservative 63; Mismatches 66; Indels 13; Gaps 2;
XX
Qy 7 SLNKSPLILHEWKFFDYDFGSDERRQDAILSGEYDYKKNYPSDIDQWHDKIFVTMLRYNG 66
Db 12 NLAHSMKVIYEWKHIDDFGSDERRDAAIKSGEFDHTKNYPFDVDRWRDKTFVTIERNG 71
XX
Qy 67 VPSSLNVISKVGDGGLLPQYPDWSFAKYDDCSGIVSASKLAIDKCDRLWVLDLSDGLVNN 126
Db 72 VPSSLNVVNNKKGGLLPQYPDWSFAKYDDCSGIVSFAKIAVDFDLWVLDLSDGLVNN 131
XX
Qy 127 TQPMCSPKLLTFDLTTSQLLKQVEIPHDAVNATTGKRLSSLAVQSLDCNTNSDTMVYI 186
Db 132 NQPMCSPKLLTFDLTTSKLKQVEIPHDAVNATTGKRLSSLAVQSLDCNTNSDTMVYI 188
XX
Qy 187 ADSKSGGLIVHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALSPMTNNL 246
Db 189 ADSKSGGLIMYQNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALSPMTNNL 248
XX
Qy 247 YVSPVASTSLVYVNTQERTSDYQONDHYEGVQNLDTQSSAKVSKSVGLFFGLVGDS 306
Db 249 YVSPVASTSLVYVNTQERTSDYQONDHYEGVQNLDTQSSAKVSKSVGLFFGLVGDS 308
XX
Qy 307 ALGCWNEHRTLERNIRTVASDETLQMIASMKIKEAXPHVPIFDRIYNREYILVLSNKM 366
Db 309 GIACVNEHQVLRSEFDDVVAQNEETLQMIVSMKIMENLQSGRINDPEGNEYMALSNRM 368
XX
```

Qy	367	QKVNDFNFDVNFVRIMNANVNELILNTRC-----ENPDN 402	
Db	369	QKIINDFNFDVNFVRILGANVDDLNRTRCGRYHNQAGNQADN 414	
RESULT 7			
ADL27616	ID	ADL27616 standard; protein; 544 AA.	
XX	AC	ADL27616;	
XX	DT	03-JUN-2004 (first entry)	
XX	DE	Honey bee RJP70.	
XX	XX	Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;	
XX	KW	royal jelly protein; allergy; pollinosis; atopic dermatitis;	
XX	KW	contact hypersensitivity; bronchial asthma; allergic rhinitis; RJP70.	
XX	OS	Apis mellifera.	
XX	Key	Location/Qualifiers	
XX	Peptide	1..20	
XX	Protein	/label= Signal_peptide	
XX	FT	21..544	
XX	FT	/label= Mature_protein	
XX	FN	WO2004019971-A1.	
XX	PD	11-MAR-2004.	
XX	XX	26-AUG-2003; 2003WO-JP010795.	
XX	PP	29-AUG-2002; 2002JP-00252087.	
XX	PR	30-JAN-2003; 2003JP-00022776.	
XX	PA	(HAYA/) HAYASHIBARA K.	
XX	PI	Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;	
XX	DR	WPI; 2004-248191/23.	
XX	DR	N-PSDB; ADL27608.	
XX	XX	Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,	
XX	PT	atopic dermatitis, contact hypersensitivity, bronchial asthma and	
XX	PT	allergic rhinitis, comprise protein originated from royal jelly.	
XX	PS	Disclosure; Page 59-62; 78pp; Japanese.	
XX	CC	The present invention relates to novel antiallergic agents, which	
XX	CC	comprise as an active ingredient, peptides ADL27604 and ADL27605, which	
XX	CC	are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606	
XX	CC	and ADL27607). The agents can be used to relieve symptoms accompanying an	
XX	CC	allergic disease e.g. pollinosis, atopic dermatitis, contact	
XX	CC	hypersensitivity, bronchial asthma and allergic rhinitis, which are	
XX	CC	applicable in foods, cosmetics and drugs. The present sequence is a honey	
XX	CC	bee RJP.	
XX	SQ	Sequence 544 AA;	
Query Match			
Best Local Similarity 65.0%; Score 1415.5; DB 8; Length 544;			
Matches 264; Conservative 63; Mismatches 66; Indels 13; Gaps 2;			
Qy	7	SLNKSPLTILHEWKFPDYDFGSDERRQDAILSGEYDKNYPDSIDQWHDKIFVTMLRYNG 66	
Db	32	NLAHMKVIYIEWKHIDPFGSDERRDAIKSGEFHTKNYPFDVDRWDRKTFVIERNG 91	
Qy	67	VPSSLNVISKVGGGGLLPYPDWSFAKYDDCSGIVSASKLAIDKCDRLWVLDGLVNN 126	
Db	92	VPSSLNVVTKKGGLLPYPDWSFAKYEDCSGIVSFAKIVDKFDRWLWLDGLVNN 151	
Qy	127	TOPMCSPKLLTLDLTTSQLLKQVEIPHDVAVNATTGKRLSSLAQSLDCNTNSDTMYVI 186	
RESULT 8			
ADL27618	ID	ADL27618 standard; protein; 544 AA.	
XX	AC	ADL27618;	
XX	DT	03-JUN-2004 (first entry)	
XX	DE	Honey bee MRJP3.	
XX	XX	Antiallergic; Antiasthmatic; Antiinflammatory; Dermatological; honey bee;	
XX	KW	royal jelly protein; allergy; pollinosis; atopic dermatitis;	
XX	KW	contact hypersensitivity; bronchial asthma; allergic rhinitis; MRJP3.	
XX	OS	Apis mellifera.	
XX	Key	Location/Qualifiers	
XX	Peptide	1..16	
XX	Protein	/label= Signal_peptide	
XX	FT	17..544	
XX	FT	/label= Mature_protein	
XX	FN	WO2004019971-A1.	
XX	PD	11-MAR-2004.	
XX	XX	26-AUG-2003; 2003WO-JP010795.	
XX	PR	29-AUG-2002; 2002JP-00252087.	
XX	PR	30-JAN-2003; 2003JP-00022776.	
XX	PA	(HAYA/) HAYASHIBARA K.	
XX	PI	Okamoto I, Arai N, Kohno K, Kurimoto M, Sano O;	
XX	DR	WPI; 2004-248191/23.	
XX	DR	N-PSDB; ADL27610.	
XX	XX	Antiallergic agents for relieving symptoms accompanying e.g. pollinosis,	
XX	PT	atopic dermatitis, contact hypersensitivity, bronchial asthma and	
XX	PT	allergic rhinitis, comprise protein originated from royal jelly.	
XX	PS	Disclosure; Page 65-69; 78pp; Japanese.	
XX	CC	The present invention relates to novel antiallergic agents, which	
XX	CC	comprise as an active ingredient, peptides ADL27604 and ADL27605, which	
XX	CC	are N-terminal peptides of honey bee royal jelly proteins (RJP, ADL27606	
XX	CC	and ADL27607). The agents can be used to relieve symptoms accompanying an	
XX	CC	allergic disease e.g. pollinosis, atopic dermatitis, contact	
XX	CC	hypersensitivity, bronchial asthma and allergic rhinitis, which are	
XX	CC	applicable in foods, cosmetics and drugs. The present sequence is a honey	
XX	CC	bee major RJP.	

```
SQ Sequence 544 AA;
Query Match 64.6%; Score 1406.5; DB 8; Length 544;
Best Local Similarity 64.8%; Pred. No. 2.1e-121;
Matches 263; Conservative 62; Mismatches 68; Indels 13; Gaps 2;

Qy 7 SLNKLPIILHEWKFDDYDFGSDERRQDAILSGEYDYKNYPSPDIDQWHDKIFVTMLRYNG 66
Db 32 NLAHSMKVIVYEWKHIIDFDFGSDERRDAAIKSGEFDHTKNYPFDVDRDXTFTVIERNN 91

Qy 67 VPSSLNISKVGGGGLLPYPDWSFAKYVSGIVSASKLAIDKCDRLWLDLSDGLVNN 126
Db 92 VPSSLNVVTKNGKGGPLLPYPDWSFAKYVSGIVSASKLAIDKCDRLWLDLSDGLVNN 151

Qy 127 TQPCSPKLLTFTDITTSQLLKQVEIPHDVAVNATTKGRLSSLAQSLDCNTNSDNTMVI 186
Db 152 NQPCSPKLLTFTDITTSQLLKQVEIPHDVAVNATTKGRLSSLAQSLDCNTNSDNTMVI 208

Qy 187 ADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALSPMTNN 246
Db 209 ADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALSPMTNN 268

Qy 247 YISPVASTSYLVNTEQFRTSDYQNDIHYEGVQNILDTQSSAKVSKSGVLPFGLVGDS 306
Db 269 YISPLLSHGLIYYVDTQFNSPQYENNVQEGSQDILNTQSGFKVSKGVLPFGLVGNS 328

Qy 307 ALGCWNEHRTLERNHIRTVAQSDETLQMIASMKIKEAXPHVIPFDRIYNREYILVLSNKM 366
Db 329 GIACVNEHQVLORESFDVAQNEETLQMIYVSMKIMENLPQSGRINDPEGNEYMLASNRM 388

Qy 367 QKVVNDFNFDVNFRIIMANVELIINTRC-----ENPDN 402
Db 389 QKIINDFNFDVNFRIIGANVDLMENTRCGRYHNQAGNQADN 434

RESULT 9
ABB60127 ID ABB60127 standard; protein; 541 AA.
XX AC ABB60127;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 7173.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX DR N-PSDB; ABL04230.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX PS Disclosure; SEQ ID NO 7173; 21pp + Sequence Listing; English.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX CC The invention relates to an isolated nucleic acid detection reagent
```

```
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 541 AA;
Query Match 20.8%; Score 452.5; DB 4; Length 541;
Best Local Similarity 30.3%; Pred. No. 1.2e-32;
Matches 125; Conservative 90; Mismatches 150; Indels 47; Gaps 17;

Qy 16 HEWKFPDYPFGSDERRQDAILSGEYDYKNYPSPDIDQWHDKIFVTMLRY-NGVPSSLNVI 74
Db 29 YWSQSLDFAPPNTRLKDQALASGDYIPQNALPGVEHFGNRLFTVPRWRDGPATLTYI 88

Qy 75 S-KKVGDDGGLLPYPDWSFAKYVDDC-SGIVSASKLAIDKCDRLWLDLSDGLV---NNTQP 129
Db 89 NMDRSLTGSPELTPYPDWSRNTAGDCANSITTAIRIKVDECGRLWLDTGTVGIGNTTN 148

Qy 130 MSCPCLLTFTDITTSQLLKQVEIPHDVAVNATTKGRLSSLAQSLDCNTN-SDTMVIYAD 188
Db 149 PCPYAVNVFDLTITTDTRIRRYELP-GVDTNPNT---FIAMIAV---DIGKNCDDAYAFAD 201

Qy 189 EKEGELIVYHNSDDSFHRLTSNTFDY-DPKFTKMTIDGESYT-AQDGISGMALSPMTNN- 245
Db 202 ELGYGLIAYSWELNKSWSRFSASHSYFPDPLRGDFNVAGINFQWGEBSIGMSLSPIRSDG 261

Qy 246 ---LYTSPVASTSYLVNTEQFRTSDYQNDIHYEGVQNILDTQSSAKVSKSGVL 298
Db 262 YRTLFPSPPLASHRQPAVSTRILRDETRTSDSVHDFVALD--ERGPSHTTSRVMSDDGIE 319

Qy 299 FFCVLGDSALGCWNEHRTL-----ERNHIRTVAQSDETLQMIASMKIKEAXPHVIPFDRIYI 354
Db 320 LFNLDIQNAVGCW--HSSMPYSQPHGI--VDRDDVGLVPADVKIDE----- 363

Qy 355 NREYILVLSNKMOKMVNDFNFDVNFRIIMANVELIINTRCENPDNDRTP 406
Db 364 -NKQVWVLSDRMPVFLSLDLYSDTNTFRIVYTAFLATLIENTVCDLRNAYGP 414

RESULT 10
ABB60071 ID ABB60071 standard; protein; 438 AA.
XX AC ABB60071;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 7005.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX CC
```



```
DR WPI; 2001-656860/75.
DR N-PSDB; ABL04174.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
PT
XX Disclosure; SEQ ID NO 7005; 2lpp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABLI16176-ABLI30511), expressed DNA
XX sequences (ABLI01840-ABLI16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 438 AA;
XX
XX Query Match 20.6%; Score 448; DB 4; Length 438;
XX Best Local Similarity 28.8%; Pred. No. 2.3e-32;
XX Matches 123; Conservative 67; Mismatches 169; Indels 68; Gaps 10;
XX
XX 18 WKFFDYFGSDERRQDAILSGEYDYKNNYPSIDIDQWHDKIFVTMLRYN-GVPSSLNVISK 76
XX ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 33 WKQLAFDWPTEAEAEAKSNHGYIVENNLPLGVQRWQNRIFVTVPWKAGVAATLNVIDI 92
XX ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 77 KVGDGGLLPQYPDWSFAK-----YDCSGIVASAK 107
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 93 NSTEKSPLKHFYPSWEANKLPIDVQPDQKTPFSGRLDADKAQAGIQLKDNSTVIFTR 152
XX
XX 108 LAIDKCDRLWLVDGLVNTQPMCSK-----LITFDLTTSQLLKQVEIPHDVAVNATT 161
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 153 IQVDVCDRLWLVDLTGLAD---ILGSPKQITNSILVFDLKTDTLLRFTIPAD-----QT 204
XX
XX 162 GKGRSLSSLAQSLDNTSNTDMVVIADKGBGLIYVHNSDDSFHRLTSNTFDYDPKFTKM 221
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 205 KEDSFFANIVDAORSECDQAFAYIPDLGAGVIVYSLRNDKSVKXHFHFPDPLHGDF 264
XX
XX 222 TIDGESYTAQDGISGMALSPM-----TNNLYSPVASTSLYVN-----TEQFRSDYQON 272
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 265 NVGGVNFQWTDGVFLGAVGPMNPDHSHKDIYFHALASTKEFKVSNRVLQNESHVITAGDSY 324
XX
XX 273 DIHVEGVQNILDTQSSAKVVS-KSGVLFGLVGDSDALGCWNEHRTLERNHIRTVAQSDET 331
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 325 DPKYVGDRG-MNGQSTAEVFDPEGVIFYTQVNDKDAIACWIKRPTPTDQGLDSDSHT 383
XX
XX 332 LQMIASMKIEXAPHPVIFDRYINREYILVLSNKMVKMNNDFNPDVYFRIMNANVNEL 391
XX ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 384 LVFPNDMKID-----NEGTLVLSDKMPTLYLKELDPSAVNVYRILMGQNRDL 430
XX
XX 392 ILNTRCE 398
XX ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 431 IKGTPCE 437
XX
XX RESULT 11
XX ABB71124
XX ID ABB71124 standard; protein; 453 AA.
XX
XX AC ABB71124;
XX
XX XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 40164.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
XX Drosophila melanogaster.
```

```
XX PN WC200171042-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 23-MAR-2001; 2001WO-US009231.
XX
XX PR 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX
XX PA (PEKE ) PE CORP NY.
XX
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX
XX DR WPI; 2001-656860/75.
XX N-PSDB; ABL15227.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 40164; 2lpp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABLI16176-ABLI30511), expressed DNA
XX sequences (ABLI01840-ABLI16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 453 AA;
XX
XX Query Match 20.0%; Score 435.5; DB 4; Length 453;
XX Best Local Similarity 28.4%; Pred. No. 3.5e-31;
XX Matches 116; Conservative 85; Mismatches 165; Indels 43; Gaps 12;
XX
XX 9 NKSIPILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSIDIDQWHDKIFVTMLRY-NGV 67
XX ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 19 NDNLRVAYEWREMDFKYANPDQWSAIERGEFKEPANVIPFGLVAGHRLFTLPRWDGV 78
XX
XX 68 PSS-----LNVISKVGDGGLLPQYPDWSFAKYDDCS-GIVSASKLAIDKCDRLWLVD- 120
XX ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 79 PASLAYLDLNDTSSK-----GPALKPFPQWQAHNIQEAPELVSPFRVADRGRGLWLVD 134
XX
XX 121 --SGLVNTQPMCSPLKLTLDLTTSQLLKQVEIPHDVAVNATTGKRLSSLAQSLDCNT 178
XX ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 135 RISGVLEQTKIYGAQQLLVYDLHNDLLRR-----HVLPAQQLKQGSLLANLAVEDSDC-- 188
XX
XX 179 NSDTMVVIADKGBGLIYVHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGM 238
XX ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 189 -ENTFAYAADLGSPLVYVSWKDESWRVQHHFHPDPMAGNFSINGIEFQWMDGLYGLA 247
XX
XX 239 LS-PWTN---NLYYSPVASTSLYVNTTEQFRTSDYQNDIHVEGVQNI---LDTQSSAK 290
XX ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 248 LSKPLETGATLYFHPPLCSTTEFSDVTSILRNKTLATSPMIYRREFKLGSGKGPFOAGAE 307
XX
XX 291 VVS-KSGVLFGLVGDSDALGCWNEHRTLERNHIRTVAQSDETLQMIASMKIEXAPHPVPI 349
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 308 FLDPDTGVLFYALPNLNEVACWRTATDFSHSSQSRHNNNDTLVFPSPDIKVDD----- 360
XX
XX 350 FDRYINREYILVLSNKMVKMNNDFNPDVYFRIMNANVNELINTRCE 398
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 361 -----QKRLVLSNQLPVIYDELYAGSINFRILTASVKEAIENTACE 403
XX
XX RESULT 12
XX ABB66147
XX ID ABB66147 standard; protein; 426 AA.
XX
XX
```



```

Db 207 GIVVDVAAQSWRI-ENKTYPHDPFGTGTIAGESFQLDWGTSTLTTHGLGGRMMY 265
Qy 248 YSPVAS-----TSLYYNTBQFRTSDYQNDIHYEGVONILD-----TSSAKVVS 293
Db 266 FHSLSSEWQMAIPLDVN-----NGSNWLND-----VSAALDQFQLGKRGSCVAAAMS 316
Qy 294 KSGVLFGLVGDSDALGQWNEHRTLERNHRTVAQSDETIQMIASMKIKEAXPHVPIFDY 353
Db 317 ESGFLICGLVQPSLLAWNRTGYSHQNLVNLVDEQRLQFASGLKIVR-----NH 367
Qy 354 INREYIIVLSNKMOMKVNNDPDDVNFNFRIMNANVNLILNTRC 397
Db 368 EGKEELWVLSNRLQAFAGGLDYKEINFRIQKCGVQELLGRPC 411

RESULT 14
ABB64727
ID ABB64727 standard; protein; 415 AA.
XX AC ABB64727;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 20973.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL08830.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX PS Disclosure; SEQ ID NO 20973; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX CC ABB72072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 415 AA;
XX Query Match 18.9%; Score 411.5; DB 4; Length 415;
XX Best Local Similarity 28.0%; Pred. No. 5.3e-29;
XX Matches 119; Conservative 74; Mismatches 147; Indels 85; Gaps 15;

Qy 5 GBSLNKSLPI-----LHEWKFFDYDFGSDERRDAILSGEYDKNNYPSDIDQWH----- 54
Db 19 GVGNGRPRVTRVETLTQWGLEFGFPPTAQDRENAQAAGNLVPENGTFIDVQPYWANGQ 78

```

```

Qy 55 DKIFVTMLRY-NGVPSLNVISKVGDGGPQLQPYD--WSFAKYDDCSGIVSASKLAID 111
Db 79 IRLFTTIPFVTVGIPYTLATVSATQGRNGPQLQPYPNYSWMHANGDCDRITSAPRAVIT 138
Qy 112 KCDRLWLVDSGLVNTOPMCSKPLTFLDTTSOLLKQVEIPHDAVAVNATTGKRL-----S 167
Db 139 ECNQMWIDSGVIGTTQ-LCPPQLQPALATDRLLHFRFPNDYIPS-----GSLFTPN 193
Qy 168 SLAVQSLDCNTNSDTWVYTADEKGEGLIVVHNSDDSPHRLTSNTDY-DPKFTKMTIDGE 226
Db 194 VLVDQPPPPRGTCSTRTMIYVADTSWR-----AENRFMPDPDYKGTIAGE 238
Qy 227 SYTAQDGISGMALSPMTNLIYSPVASTSLYYVN-----TEQFRTSDY 269
Db 239 SFYLMGDM--FALNDKRNLYFHLASASEYSVPLSALNRQONWANGPEALPEEFRLGR 296
Qy 270 QQNDIHYEGVONILDQTSSAKVSKGVLPFGLVGDALGCVNEHRTLERNHRTVAQSD 329
Db 297 RRS-----ECAAASAIIDGRNNVYCVTFNPKLF-----VMVNSPYNSRNFGLNPAKS 343
Qy 330 ETLOMTASMKIKEAXPHVPIFDYINR---EYILVLSNKMOMKVNNDPDDVNFNFRIMNA 386
Db 344 DDLQFVSGMKVLR-----NREGQBELMULSNRYOKIAAGTINSKEVNFRLRR 391
Qy 387 NVNEL 391
Db 392 KLDDV 396

RESULT 15
ABB67082
ID ABB67082 standard; protein; 429 AA.
XX AC ABB67082;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 28038.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL11185.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX PS Disclosure; SEQ ID NO 28038; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

```

```
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 429 AA;
Query Match 16.8%; Score 366; DB 4; Length 429;
Best Local Similarity 27.6%; Pred. No. 9.5e-25;
Matches 105; Conservative 68; Mismatches 169; Indels 38; Gaps 12;
Qy 37 SGEYDYKNNYPSDIDQHQHDKIFVTM-LRYNGVPSSLNVI--SKKVGSGPILLQYPDPWSF 93
Db ||| : ||| : : : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
70 SGSEFIQNNYVPGQVTHFRGRLEFVTPRRQPCIPSTLNYIDLAKDQNSQSPHLRAYPNLAV 129
Qy 94 AKYDDC-SGIVSASKLAIDKCDRLWLDGLV---NNTQPMCGPKLITFDLTTSQLKQV 149
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
130 NQYNASEQNLVSVYRTSDVCGRLWFVDTGMLFPPNRRQQIRHPSIWIIDLANDRLLRKF 189
Qy 150 EIPHDVAVNATTGKGRLS-SLAVQSLDCNTNSDTMVIYIADEKGEGLIVYHNSDDSFHRLT 208
Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
190 EIPQSI--VEIGRGLASITIDVGARRCN--DAYAVIPDLVNRRLHVYHLRSDRIWSFE 243
Qy 209 SNTFDYDPKFTKMTIDGESYTAQDGISGMALSPM----TNNLYYSPVASTSLYYVNT--- 261
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
244 HSFNFDPDLSNLIIGQTFRWDGIFSATLGSYKPDGSRDVFPHPMASTNEFVVSNRVL 303
Qy 262 -EQFRT--SDYQONDHYEGVQNIQSSAKVVSXGVLFFGLVGDGSAALGCWNEHRTLE 318
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
304 QQEFNAARSDH-GDDFHLGTRGPSTOSTWHKYDPRGVIFFAEVQKSGVGCWTKSPFS 362
Qy 319 RHNIRTVAQSDETLQMIASMKIEAPHPVIFDRIYNREYILVLSNKMQRWVNDNFDD 378
Db :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
363 TENHGSVYSNSSEMIYPSDLTIDE-----EGYIWMNSMMPIFVYSKLDVEK 409
Qy 379 VNFRIANVNELILNTRCE 398
Db |||| : |||
410 YNFRIMRQSTLLAKRGTVCE 429
```

Search completed: May 3, 2006, 19:01:18
Job time : 179.482 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:01:48 ; Search time 31.0175 Seconds
(without alignments)
1281.133 Million cell updates/sec

Title: US-10-525-567-4
Perfect score: 2178
Sequence: 1 NIIRGSLNKLSPILHWEK.....NTRCENPDNDRTPFKISLH 413

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1347.5	61.9	467	2 S39193	royal jelly protei
2	1216.5	55.9	464	2 S39194	royal jelly protei
3	452.5	20.8	541	2 A25696	yellow protein - f
4	435.5	20.0	453	2 J7253	Yellow-B protein -
5	179.5	8.2	388	2 D75353	yellow-related pro
6	114	5.2	340	2 T22741	hypothetical prote
7	114	5.2	414	2 D86764	hypothetical prote
8	113.5	5.2	1530	2 AH1396	peptidoglycan anch
9	112.5	5.2	1252	2 S21178	botulinum neurotox
10	111	5.1	1088	2 B34106	protein kinase (EC
11	110.5	5.1	1251	2 JH0256	botulinum neurotox
12	110	5.1	2178	2 S55805	alpha-toxin - Clos
13	109.5	5.0	1120	2 H71664	transcription-repa
14	109	5.0	4688	2 F82885	hypothetical prote
15	107.5	4.9	1516	2 E71619	RAD2 endonuclease
16	104	4.8	463	2 T33992	hypothetical prote
17	103.5	4.8	934	2 T08418	protein kinase (EC
18	103.5	4.8	1132	2 H82887	hypothetical prote
19	103	4.7	875	2 S70115	ZIP1 protein - yea
20	103	4.7	3562	2 A47171	chondroitin sulfat
21	102	4.7	446	2 S67437	Damage and replica
22	101	4.6	888	2 E82885	hypothetical prote
23	101	4.6	2229	2 T16199	hypothetical prote
24	100.5	4.6	345	2 A97113	probable Fe-S-clus
25	100.5	4.6	997	2 S73556	MG414 homolog C12
26	100.5	4.6	1162	2 A47708	progenitor toxin n
27	100.5	4.6	2314	1 A46151	protein-tyrosine-p
28	100	4.6	721	2 T05815	hypothetical prote
29	99.5	4.6	589	2 B97806	hypothetical prote

30	99.5	4.6	2496	2 A71616	secreted protein P
31	99	4.5	1112	2 T06307	hypothetical prote
32	98.5	4.5	412	2 C83531	aspartate kinase a
33	98.5	4.5	428	2 S15662	farnesyltransferas
34	98.5	4.5	452	2 S15662	sugar-binding peri
35	98.5	4.5	641	2 E82884	DNA primase UU494
36	98.5	4.5	1217	2 F97177	alpha-glucosidase
37	98.5	4.5	2026	1 OYBY	adenylate cyclase
38	98	4.5	595	2 E82934	hypothetical prote
39	97.5	4.5	796	2 S66769	probable membrane
40	97.5	4.5	1047	2 T14897	probable ATPase (E
41	97.5	4.5	1198	2 T34340	dynamin heavy chain
42	97.5	4.5	1608	2 T17201	adenylate cyclase
43	97.5	4.5	1795	2 F97713	190K antigen precu
44	97.5	4.5	1902	2 C97702	cell surface antig
45	97.5	4.5	2140	2 P95074	serine proteinase,

ALIGNMENTS

RESULT 1

S39193
royal jelly protein RJP57-1 - honeybee
C;Species: Apis mellifera (honeybee)
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 12-May-1995
C;Accession: S39193
R;Klaudiny, J.; Hanse, J.; Kulifajova, J.; Albert, S.; Simuth, J.
A;Submitted to the EMBL Data Library, September 1993
A;Description: Molecular cloning of two cDNAs from the head of the nurse honey bee (Apis mellifera) encoding a protein that is highly homologous to the honeybee protein RJP57-1.
A;Reference number: S39193
A;Accession: S39193
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-467 <KLA>
A;Cross-references: UNIPARC:UPI0000179A48; EMBL:Z26318

Query Match 61.9% Score 1347.5; DB 2; Length 467;
Best Local Similarity 63.3%; Pred. No. 5e-93;
Matches 257; Conservative 62; Mismatches 72; Indels 15; Gaps 4;

Qy	7	SLNKLSPILHWEKFPDYDFGSDERRQDAIISGEYDYKKNYPSPSIDQHKDKIFVTMLRYNG	66
Db	32	NLAHSMKVIVYEWKHIDFDGSDEREM-LRLNLRIDHTKNY-FDVRWRDKFTVTIERNNG	89
Qy	67	VPSSLNVIKKGVDGCGPILQYPDPWSFAKYDCSIVSASKLAIDKCDRLWVLDSGLVNN	126
Db	90	VPSSLNVTNKKGGKGLLPYPDPWSFAKYDCSIVSAPKIAVDKFDRLWVLDSGLVNN	149
Qy	127	TOPMCSPLLTFTDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNSDTWYI	186
Db	150	NQPMCSPLLTFTDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNSDTWYI	206
Qy	187	ADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTQMTIDGSGYTAQDGISGHALSPMTNNL	246
Db	207	ADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTQMTIDGSGYTAQDGISGHALSPMTNNL	266
Qy	247	YISPVASTLSLYVNTQFRTSDYQNDIHIEGVQNIIDTQSSAKVSKSVGLFGLVGDS	306
Db	267	YISPLLSHGLYVYVTEQFSNPQYBENNVOYEGSDIILNTQSFQKVKVSKNGVLFGLVGNS	326
Qy	307	ALGCMWNEHRTLERINIRTVAGSDSETLOMIASMKIKEAPHVPIPDFYINRYEIVLSNKM	366
Db	327	GIACNHHQVLRQSFQVDAQNEETLQIVSMKINENLQSGRINDEPGEYMLALSIRM	386
Qy	367	QKWNNDNFDDVNFIRMANVNLIILNTRC-----ENPDN 402	
Db	387	QKIINDDNFNDVNFIRLGANVDDLMRNTCRGRVYHQNQAGNQADN 432	

RESULT 2

S39194
royal jelly protein RJP57-2 - honeybee

Db 189 -ENTFAVAADLGSGLVVYVSKDESRVQHFFHPDPMAGNFSINGIERQWDDGLYGLA 247

Qy 239 LS-EWNTN---NLXYSPVASTSLYYVNTQEQFTSDYQQNDIHVEGVQNI-----LDTQSAK 290

Db 248 LSKPLETGATLYFHPPLCSTTEPFSVDTSILRNKTKLATSPMIYRFBKVLGSRGPNTOAGAE 307

Qy 291 VVS-KSGVLPGLVGDSDALGCMWNEHRLERHNIRTVASQDBTLQMIASMKIEXPHVPI 349

Db 308 FLDPDTGVLFPALPNLNEVACWRTATDFSHSQSQRIHNNNDTLVPFSDIKVDD----- 360

Qy 350 FDRVINREYILVLSNKKQKMNNDNFDDVNFIRIMNANVNLEILNTRCE 398

Db 361 -----QKRLWLSNQLPVFIYDELYAGSINFRILTASVKEAIENTACE 403

RESULT 5

D75353

Yellow-related protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: D75353

R:White, O.; Eise, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: D75353

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-388 <WIL>

A:Cross-references: UNIPROT:Q9RTH4; UNIPARC:UPI00000D3ED5; GB:AE002021; GB:AE000513; NID

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR1790

A:Map position: 1

Query Match 8.2%; Score 179.5; DB 2; Length 388;

Best Local Similarity 22.7%; Pred. No. 8.6e-06;

Matches 88; Conservative 57; Mismatches 133; Indels 109; Gaps 18;

Qy 50 IDWDHDKIFVTMLRYNGVPSSILNISKVGDGGLLPQYPDWSPAKYDDC----- 99

Db 31 VSAAGKLEVVHRFYGHMPIGVTVNSQ-----GRMFVSYPWE-----DDVFSIAEIKGG 81

Qy 100 -----SGIVSASKLAIDKCDRLWLVDLSGLVNNTPMC---SPKLIT 137

Db 82 REVYPNRAINTRDLSKPDPTTFIGVGLLVDAARDLWLDTG-TRNLGPILDQRAVKLVG 140

Qy 138 FDLTTSQLLKQVEIPHDVAVNATTKGRLSSLAQSLDNTNNTWVIAD---BKGEGL 194

Db 141 IDHTNEVVKTIHFPADVALKNT---YLNDLRI---DLROGTGGVAYITDSGAKSGSL 193

Qy 195 IYVH-NSDDSFRLTSN-TFDYDPKFTKMTIDGESYTAQD-----GISGMALSPM 242

Db 194 IYVDLASGSKWRKLGDTEVDPVPGFVPY-VEGQALFORPKGPGPATHLGFAGDLSAISPD 252

Qy 243 TNNLYSPVASTSLYYVNTQEQFTSDYQQNDIHVEGVQNIQSSAKVSKSGVLPFGL 302

Db 253 GATLYAPATSRRLVAVPTAALRD-----QGLSD-AEVKKQKXDLGEGAA-DGL 300

Qy 303 VGDSALGCWNEH-----RTLERNIRTVASQ-----DETQMTASMKIEXPHVPIF 350

Db 301 AEDTAGNIYITNVEQCALVRRLPTGELQTLARDPRLIWPDTLA----- 343

Qy 351 DRYINREYILVLSNKKQKMNNDNFDDVNFIRIMNANVNLEILNTRCE 377

Db 344 ---IQGSYLYVLNDQLNRQGGYHFGKD 367

RESULT 6

T22741

hypotheical protein F55G11.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T22741

R:Baynes, C.

A:Reference number: Z19608

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Accession: T22741

A:Molecule type: DNA

A:Residues: 1-340 <WIL>

A:Cross-references: UNIPROT:Q9XUEI; UNIPARC:UPI000000790CC; EMBL:Z82272; PIDN:CAB05215.1;

A:Experimental source: clone F55G11

C:Genetics:

A:Gene: CESP:F55G11.6

A:Map position: 4

A:Introns: 21/1; 97/2; 134/1; 200/2; 239/1; 287/3; 308/2

Query Match 5.2%; Score 114; DB 2; Length 340;

Best Local Similarity 24.3%; Pred. No. 0.56;

Matches 76; Conservative 33; Mismatches 98; Indels 106; Gaps 18;

Qy 72 NVISKVGDGGLLPQYPDHS-----PAKYDDCSGIVSA-----SKLAI-----DKCD 114

Db 26 NVINKPIDGTVPVYWP-PSWTETQAPQLDKEOSCSWIVTIPRGYYAKLIISGKTTDKDS 84

Qy 115 RLWLIDS--GLVNNTPCMCKPCLL---TFDLTTSQLLKQVEIPHDVAVNATTKGRLSSL 169

Db 85 RFQTVDSAGNLIQTTQENMDPYFPFASKFLAVS-----NEGSATPAFK 128

Qy 170 AVQSLDCNTNSDTMWYIADKSG---EGLIV-----YHNSDDSFRLTSNTFDYDP 216

Db 129 VVWFL-----LPYVGDDAGIGPSGLVNVNTSKVYADYHSTDD---LTLMTFPADT 177

Qy 217 KFTKMTIDGESYTAQDGI--SGMALSPMNNLYSPVASTSLYYVNTQEQFTSDYQQNDI 274

Db 178 K-----NYYLSRSALVFAGEGLSNITNLY-----LLYQTKKPMWISSDDAITIV 221

Qy 275 HYEGV---QNILDTQSS-----AKVWSKGVLPFGLVGDSDALGCMWNEHRLERHNI 322

Db 222 NFEAASNDNLL-IQSSKYLTIQEMVELHPQANSIYNGTVNGGTL-----MS 268

Qy 323 RTVAQSDDELQMI 335

Db 269 SLVAVTDLPMQMI 281

RESULT 7

D86764

hypotheical protein ylcF [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C:Accession: D86764

R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, J.; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich, J.

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss

A:Reference number: R86625; MUID:21235186; PMID:11337471

A:Accession: D86764

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-414 <STO>

A:Cross-references: UNIPROT:Q9CGI0; UNIPARC:UPI00000D4431; GB:AE005176; PID:gl2724076; F

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: ylcF

Query Match 5.2%; Score 114; DB 2; Length 414;

Best Local Similarity 24.9%; Pred. No. 0.75;

Matches 56; Conservative 32; Mismatches 60; Indels 77; Gaps 12;

Qy 232 DGISGMALSPMNNLYSPVASTSL-----YYVNTQEQFTSDYQQN-----DIHVEGV- 279

Db 206 EGITGY----IAKNTVVLRIADSNLINGSYVLTNFR--DYEQNIQELIAKTABEEGL 259

Qy 280 -QNILDTQSSAKVKSGLVFPGLVGDAL-----GCWNE----- 313
Db 260 RENILCAGSSR---GGMGALYHGLGNALVSMDDPVVDRSPFLQSGADVDQMFDCIPVSFV 316
Qy 314 --HRTLEHNRITVAOSDEFLQMIASMKIKEAAXPHVPIFDYINREYILVLSNKMOMV 370
Db 317 DKLNLLEKTNL-----SAEKIQVITS-----PQPIYTFPIQIKWKLALKTYRMK 364
Qy 371 NNDNFDP-----DVNFRIMANNVNELNTRCENPDN 402
Db 365 LTDRQFDYQPYGGRKHGDFVNRNPIPLLLMKINEFLYG--CDSTEN 407
RESULT 8
AH1396
peptidoglycan anchored protein (LPXTG motif) [imported] - Listeria monocytogenes (strain
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1396
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueder, T.; Simoes, N.; Tierrez, A.; Vasquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1396
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1530 <GLA>
A;Cross-references: UNIPROT:Q8V479; UNIPARC:UPI0000054CB4; GB:NC_003210; PIDN:CAD00654.1
A;Experimental source: strain BGD-e
C;Genetics:
A;Gene: lmo2576
Query Match 5.2%; Score 113.5; DB 2; Length 1530;
Best Local Similarity 20.8%; Pred. No. 5.6;
Matches 106; Conservative 79; Mismatches 182; Indels 143; Gaps 32;
Qy 3 LRGSLSNKLSPILHEW-KFFDYDFGSDERRQDAI-----LGSYDYDKNN----- 45
Db 522 LNGDS-----SWKGFQINFNRDITGQHVITYKTQNPSTHTSGDNEYTNNAIKT 572
Qy 46 ---YPSDID-QWHDKIFVTMLRYNGVPSLSNLSKVKGDGGLQPYPDWSPFAKYDPCSG 101
Db 573 DTAESDSDTKWIDKVIDADGKNG-----VFNKKTGE-----IEWKLI-FNDSK 617
Qy 102 IVSASKLAID---KCDRLWVLDGLVNTQPMCSPKI-----LTFPLT-----TSOL 145
Db 618 LI--SKPTIEDLSNLSGQTFTQDSIEHKIDLSATPQVGELIPPNYDVTFKKGNGEQM 675
Qy 146 LKQVEIP--HDVAVNATT-----GKRLSSLAVQSLDNTNSDTMWY 185
Db 676 LITFKKPLIHPEVITYKTKPVGIIKPKYKQKAVISDGEVLADYEAVIDDNANK-----Y 731
Qy 186 I---ADEKGEGL---IVYHNSDPSRLTSNTFDYDPKTKMTIDGES---YTAQDGISG- 236
Db 732 VNKSGEQVDNIDWEIVANQSGS---TVSNATVTDTLTGQKLDTSIIKVKYSQTSVTGK 788
Qy 237 -----MALSPMTNLYSPVASTSLYVNTQRTSDYQONDHYE-GVQNILDTQSSA 289
Db 789 MLQESNMPIPSGEYDLTKTGVDSEENLEYFQV-KFKNBINSQYVIKYQTATLTLSDTETTA 847
Qy 290 KWSKSGVLPFGLVGDGSLGALGCMWNRHRLERHIRT-VAQSD-----ETLOWIASMKIKEA 343
Db 848 QI--GNSVTF---TGDNI-----TKGETKYNIEVKITGTGCTGTGKIILN-KYDKA 897
Qy 344 XPHVPI----FDYINREYILVLSNKMOMV-NDFNPDVNFIMMANVNELILNTRCE 398
Db 898 DPSIPLEGATPDLYANDEKVDVTDQTDKNGVIEFDLVGYDYLKVEVSAPEGYTLPTASTE 957
Qy 399 NPD-----NDRTPFKIS--IHL 413

Db 958 NIOVKLEQDEKVVQVWNRKPKIKETGEVHL 987
RESULT 9
S21178
botulinum neurotoxin type E precursor - Clostridium botulinum
C;Species: Clostridium botulinum
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C;Accession: S21178; S48107; JH0257; B35294; A60027; S18111
R;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Atkinson, T.; Minton, N.P.
Eur. J. Biochem. 204, 657-667, 1992
A;Title: The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin,
A;Reference number: S21178; MUID:92174922; PMID:1541280
A;Accession: S21178
A;Molecule type: DNA
A;Residues: 1-1252 <WHE>
A;Cross-references: UNIPROT:Q00496; UNIPROT:Q45862; UNIPARC:UPI0000010A3; EMBL:X62683; J
R;Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A;Title: Gene probes for identification of the botulin neurotoxin gene and specific ide
A;Reference number: S48103; MUID:94013372; PMID:8408542
A;Accession: S48107
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 616-982 <CM>
A;Cross-references: UNIPARC:UPI000008CF0; EMBL:X70815; NID:9407786; PIDN:CAA50146.1; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
Biochem. Biophys. Res. Commun. 183, 107-113, 1992
A;Title: Sequences of the botulin neurotoxin E derived from Clostridium botulinum type
A;Reference number: JH0256; MUID:92181428; PMID:1543481
A;Accession: JH0257
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-176, 'R', 178-197, 'C', 199-339, 'R', 341-772, 'I', 774-962, 'FE', 965-966, 'R', 968-11
A;Cross-references: UNIPARC:UPI000016EA7F; EMBL:X62089; NID:940393; PIDN:CAA43999.1; PID
A;Experimental source: strain Beluga
R;Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.
J. Biol. Chem. 265, 9153-9158, 1990
A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other
A;Reference number: A35294; MUID:90264400; PMID:2160960
A;Accession: B35294
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-176, 'R', 178-252 <BIN>
A;Cross-references: UNIPARC:UPI000017670F
A;Experimental source: strain Beluga
R;Gimenez, J.A.; DasGupta, B.R.
Biochimie 72, 213-217, 1990
A;Title: Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the sit
A;Reference number: A60027; MUID:90344918; PMID:2116911
A;Accession: A60027
A;Molecule type: protein
A;Residues: 420-427 <GIM>
A;Cross-references: UNIPARC:UPI0000176710
A;Experimental source: strain Beluga
A;Note: this fragment was generated by proteolysis with Lys-C rather than with trypsin
C;Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit neu
C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the lig
C;Keywords: neurotoxin
F;1-422/Product: botulinum neurotoxin type E light chain #status predicted <LCH>
F;423-1252/Product: botulinum neurotoxin type E heavy chain #status predicted <HCH>
F;412-426/Disulfide bonds: #status predicted
Query Match 5.2%; Score 112.5; DB 2; Length 1252;
Best Local Similarity 20.3%; Pred. No. 4.9;
Matches 96; Conservative 83; Mismatches 173; Indels 121; Gaps 26;
Qy 1 NILRGSLNKLSPF-----LHEWKFYDFGSDERRQALLSGEYDYKQNPDSI 50
Db 414 NIVSVKGIRKISICIEINNGELFFVASENSYNDONINPTKPIDDTVTS-----NNNYENDL 468

Query Match 5.1%; Score 111; DB 2; Length 1088;
Best Local Similarity 20.6%; Pred. No. 5.2;
Matches 103; Conservative 68; Mismatches 156; Indels 172; Gaps 25;
QY 3 LRGESLNKSLPIELHEWKFFDYDFGSDERRQDAILSGEYDYKNTVPDSIDQWHDKIFVTML 62
481 ISARPOSSSLULHEVSPKPYD-KDERSRELLIKAAILD--NDPWNKMLDTQIREIVDCM 536

Query Match 5.1%; Score 110.5; DB 2; Length 1251;
 Best Local Similarity 20.1%; Pred. No. 6.9;
 Matches 96; Conservative 83; Mismatches 168; Indels 131; Gaps 27;
 Qy 1 NILRGESLNKSLPI-----LHWKFFDYDFGSDERRQDAILSGEVDYKKNYPSDI 50

301 FYTLGPTSLYF--TASATIELLEQKNILISVENSEQASLIGNISISF--LEKTIPTD 356
182 TWVYIADEK-GEGLIVVHNSDDSFHRLTSNTFYDPKFTMTTIDGSGYTAQDGGISGMS 240
357 KLFELIKANPHKIIICSSVLSSFERIKSIQNVETFEINKLDE---AKASVINIGII 413
241 PMTNLY---YSPVASTSL---YYNT----- 261
414 PLNQSFYTKYFLFITSSELEKTYLNTNKKLKNILLELDNKBGEFVVKHGHGIGQFL 473
262 --BOFTSD-----YQNDIHVEGVONILDTQSSAKVSKSGVLFFGLVGDSA--- 307
474 KLEAFKIQGLHDFKILYFGNDKLYPVVENI-----EVIKYG-----SDNAELN 519
308 -LG--CWNEHRTLERNIRTVASDETLQMIASMKIEXA---HVPIDFYI-----N 355
520 KLGSAVWAKSKAKLKNRIKEI--SLHLIQIAAKRKLMIPTIELDLEAYDKFCANFPFSE 577
356 REVILVLNKKQKQKVNDFNFD-----DVNF 381
578 TEBQLTAINDIREDLTNGMLMDRLICGDVGF 608

RESULT 14
F82885
hypothetical protein UUA482 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: F82885
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to Genbank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: F82885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4688 <GLA>
A;Cross-references: UNIPARC:UPI0000110213; GB:AE002145; GB:AF222894; NID:96899476; PIDN:
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UUA482
A;Genetic code: SGC3

Query Match 5.0%; Score 109; DB 2; Length 4688;
Best Local Similarity 17.6%; Pred. No. 62;
Matches 87; Conservative 64; Mismatches 169; Indels 174; Gaps 20;
28 DERQDAILSG-----EYDYKNYPSPDIDQWHDKIFVTMLRYNG----- 66
1824 DKKEYNLVLNKLKPGRRYSLKKNIKKEVDNGQDHEFVKKEINVNNSFDVNLQSEITASSVE 1893
67 -----VPSSLNVISGKVGDDGGLLPQYPDWSFAKYDDCSGIVASAKLAIDKCDRLWLDS 121
1884 EINDRAPDKLQNTIKI-----NLKODNDILKTDIATIDYNEQKVA 1927
122 GLVNTQPMCSPLKLTDFLTSSQLLKQVEIPHDVAVNATTKGRLSSVLAVOSLDCNTSD 181
1928 IVKNTAQ---NOKYLEAITNLVFNKNVIK-----KIEFKNLSTQFIKVGKNNT 1974
182 TWVYIADEKGEGLIVYHN-----SDD-----SFHRLTSNTFDY---DPKFTK-- 220
1975 NVIY--DESNLKLINNDFOIIGPLSTDVNSTQNVANNKHVISSTLDKFNPHISKNL 2032
221 -----WTIDGESYTAQDGGISGMSLSPMTNNLYSPVASTSLYYVNTTEQ-----FRTSDYQ 270
2033 KFKLKFQNINGE-----VVTSPILTNSIIIVNNKKNVINTLNLK 2073
271 QN-----DIHY-----EGVQNIQDQSSAKVSKGVLFFGLVGDSA 307
2074 SNQLYRLVDVYIDNNDTINDKNKPVANNVTRIIDIAPGKTTISKN----- 2122
308 LGCWNEHRTLERNIRTVASD-----ETLQMIASMK-----I 340

2123 -NTWNTTSSQPEF--VINSDDGNEVLNLEATISFKKGQTLTTFVKVNIKONNKYLI 2179
341 KEAXPHVPIFDYINREYILVLSNKKQK--WVANDNFDDVNPFRIMANVNELILNTRCEN 399
2180 KGOITNLEPENRYVLESILLAKPNKTKPLVVEILNKLDDISFQTAGNYK--VQIKSQN 2237
400 PNDRTPFKISIH 413
2238 PSTVDTKQRIKLKL 2251

RESULT 15
E71619
RAD2 endonuclease PFB0265C - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Accession: E71619
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: E71619
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1516 <GAR>
A;Cross-references: UNIPROT:O96154; UNIPARC:UPI000007D036; GB:AE001383; GB:AE001362; NID
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0265C

Query Match 4.9%; Score 107.5; DB 2; Length 1516;
Best Local Similarity 20.6%; Pred. No. 15;
Matches 84; Conservative 69; Mismatches 141; Indels 113; Gaps 18;
9 NKSPLILHEWKFPDYDFGSDERRQDAILSGEYDYKN--YPSDIDQWH--DKIFVTMLR- 63
848 NKSLS-----YEDGENFITRNEPITNEYBEKNIIYISDEQYNEEDIIIPKDKIKE 897
64 --YNGVPSSLNV-----ISKVGGGGLLPQYPDWSFAKYDDCSGIVASAKLAI----- 110
898 KEXNNDTSSDDFENCVSQEKI-----YVNEKIEEYNNKNDKSSSSSIILEBIKY 948
111 --DKCDELWLVDLSGLVNNTPQMCSPKLLTFDLTSSQLLKQVEIPHD-----VAVNATTKG 163
949 KKEKKDEL-----VSPNLCV-----LDFEHSNDLNNYISVSSDDMK 987
164 GRSSSLAVQSLDCNTNSDTMVYIADKGEGLIVVHNSDDSFHRLTSNTFDYDPKFTKWTI 223
988 TNVSKNNTGVKENKVDKTNVEY-DKGGDGVIEISFEDS-HKLEESKFDDNNNIYDND 1045
224 DGSYTAQDGGISGMSLSPMTNNLYSPVASTSLYYVNTTEQFRTSDYQNDIHVEGVQNIL 283
1046 ELEKNLSKDYISDVKNHV-NNIY-----NIE--RGEDEREN-----BFVENKI 1086
284 DTQSSAKVSKSGVLFFGLVGDSALGCMWNEHRTLERNIRTVASDDETLQMIASMKIKEA 343
1087 QSTESHKS-----NEFICTENSLRKQYMSKEDISNVRILKSDD- 1125
344 XPHVPIFDYINREYILVLSNKKQKQKVNDFNDFDVFNFRIMANVNE 390
1126 -----INNLSKNYFEILLDKKQVMDNFQNNIEQNNDKLKEDKLDE 1166

Search completed: May 3, 2006, 19:10:12
Job time : 35.0175 secs

This Page Blank (usps)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 18:54:38 ; Search time 191.204 Seconds

(without alignments)
1523.941 Million cell updates/sec

Title: US-10-525-567-4

Perfect score: 2178

Sequence: 1 NIIRGSLNKSUPILHEWKF.....NTRCENPDNDRTPFKISIH 413

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2177	99.9	432	1	MRJPI1 APIME
2	2177	99.9	432	2	Q548D6 APIME
3	2023	92.9	433	2	Q8MMJ1 APICE
4	2020	92.7	433	2	Q5VLE2 APICE
5	1454.5	66.8	443	2	Q6IMJ9 APIME
6	1441	66.2	452	1	MRJP2 APIME
7	1411	64.8	463	2	Q8MMJ0 APICE
8	1411	64.8	463	2	Q50H66 APICE
9	1411	64.8	468	2	Q5VK55 APICE
10	1406.5	64.6	544	1	MRJP3 APIME
11	1401	64.3	437	2	Q6W383 APIME
12	1354	62.2	579	2	Q6QN15 APICE
13	1343.5	61.7	598	2	Q5VK56 APICE
14	1300.5	59.7	598	1	MRJP5 APIME
15	1282	58.9	485	2	Q6QNT6 APICE
16	1273.5	58.5	416	2	Q6TGR0 APIME
17	1216.5	55.9	464	1	MRJP4 APIME
18	1190	54.6	423	2	Q4ZJX1 APIME
19	1053	48.3	222	2	Q51224 APICE
20	806.5	37.0	222	2	Q51222 APICE
21	781	35.9	220	2	Q51223 APICE
22	508	23.3	463	2	Q9V4C0 DROME
23	492	22.6	406	2	Q7Q4T5 ANOGEA
24	466.5	21.4	461	2	Q7PHB5 ANOGEA
25	464	21.3	497	2	Q7Z0H1 9DIPT
26	463.5	21.3	540	2	Q86CU0 9DIPT
27	462.5	21.2	541	1	YELL DROVA
28	462.5	21.2	541	2	Q8ISG5 DROVI
29	461	21.2	494	2	Q7Z0H2 9DIPT
30	458.5	21.1	546	2	Q5IBN4 9DIPT
31	455.5	20.9	411	2	Q6DLY9 APIME

RESULT 1

MRJPI1 APIME STANDARD; PRT; 432 AA.

AC O18330; 20.8 453 20.8 462 2 Q7PMG1 ANOGEA
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Major royal jelly protein 1 precursor (MRJP-1) (Bee-milk protein).
 GN Name=MRJP1;
 OS Apis mellifera (Honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apoidea; Apoidea;
 OC Apidae; Apis.
 OC NCBI_TaxID=7460;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 39-48; 63-71 AND 361-380.
 RC TISSUE=Hypopharyngeal gland;
 RX MEDLINE=98055707; PubMed=9395329;
 RA Ohashi K., Natori S., Kubo T.;
 RT "Change in the mode of gene expression of the hypopharyngeal gland
 RT cells with an age-dependent role change of the worker honeybee Apis
 RT mellifera L.";
 RL Eur. J. Biochem. 249:797-802(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 20-30.
 RC TISSUE=Head;
 RX MEDLINE=99007754; PubMed=9791542; DOI=10.1007/s000180050229;
 RA Schmitzova J., Klaudivny J., Albert S., Schroeder W., Schreckengost W.,
 RA Hanes J., Judova J., Simuth J.;
 RT "A family of major royal jelly proteins of the honeybee Apis mellifera
 RT L.";
 RL Cell. Mol. Life Sci. 54:1020-1030(1998).
 CC -!- FUNCTION: May play an important role in honeybee nutrition. Most
 CC abundant protein found in the royal jelly which is the food of the
 CC queen honey bee larva. The royal jelly determines the development
 CC of the young larvae and is responsible for the high reproductive
 CC ability of the honeybee queen.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Found in the hypopharyngeal glands of the
 CC worker honeybee.
 CC -!- DEVELOPMENTAL STAGE: Produced in the cephalic glands of both the
 CC nurse bee and the forager bee. This bee milk protein changes to
 CC alpha-glucosidase in accordance with the age-dependent role change
 CC of the worker bee.
 CC -!- SIMILARITY: Belongs to the major royal jelly protein family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 DR EMBL; D79207; BAA23639.1; -; mRNA.
 DR EMBL; AF000633; AAC61895.1; -; mRNA.

ALIGNMENTS

Q7PMG1 anopheles g
 P62408 drosophila
 P09957 drosophila
 P62407 drosophila
 Q9bi23 drosophila
 Q9gp81 drosophila
 Q7kw37 drosophila
 Q9vjg3 drosophila
 Q9gp71 drosophila
 Q9bi26 drosophila
 Q9bi18 drosophila
 Q9wlrl drosophila
 Q02437 drosophila
 Q9vj15 drosophila

```
DR Ensembl; ENSAPMG0000007331; Apis mellifera.
DR InterPro; IPR009007; Pept_Asparc_cat.
DR InterPro; IPR003534; Royaljelly.
DR PANTHER; PTHR10009; Royaljelly; 1.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW Direct protein sequencing; Glycoprotein; Signal.
FT SIGNAL 1 19
FT CHAIN 20 432 Major royal jelly protein 1.
FT CARBOHYD 28 28 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 144 144 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 177 177 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 432 AA; 48886 MW; 9F42BF08D34A1A7B CRC64;

Query Match 99.9%; Score 2177; DB 1; Length 432;
Best Local Similarity 99.8%; Pred. No. 5.9e-151;
Matches 412; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NILRGESLNKSLPILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSDIDQWHDKIFVT 60
DB 20 NILRGESLNKSLPILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSDIDQWHDKIFVT 79

QY 61 MLRYNGVPSSLNVISKVGSGPLLOPYPDWFAKYDDCGSIVSASKLAIDKCDRLWVLD 120
DB 80 MLRYNGVPSSLNVISKVGSGPLLOPYPDWFAKYDDCGSIVSASKLAIDKCDRLWVLD 139

QY 121 SGLVNNTPQMSCPKLITFDLTTTSQLKQVEIPHDVAVNATTGKGRSSLAQSLDCNTNS 180
DB 140 SGLVNNTPQMSCPKLITFDLTTTSQLKQVEIPHDVAVNATTGKGRSSLAQSLDCNTNS 199

QY 181 DTWVYIADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALS 240
DB 200 DTWVYIADEKGEGLIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALS 259

QY 241 PMTNLYYSPVASTSLYYVNTQFRTSDYQONDIHYEGVQNILDTOSSAKVSKGVLPFF 300
DB 260 PMTNLYYSPVASTSLYYVNTQFRTSDYQONDIHYEGVQNILDTOSSAKVSKGVLPFF 319

QY 301 GLVGDSALGCWNEHRTLERNIRTVQAQSDETLQMIASMKIKEALPHVIPFDRIYINREYIL 360
DB 320 GLVGDSALGCWNEHRTLERNIRTVQAQSDETLQMIASMKIKEALPHVIPFDRIYINREYIL 379

QY 361 VLSNKKQKQVNNDFNFDVNFIRMANVNELIINTRCENPDNDRTPFKISIH 413
DB 380 VLSNKKQKQVNNDFNFDVNFIRMANVNELIINTRCENPDNDRTPFKISIH 432

RESULT 3
Q8MMJ1 APICE
ID Q8MMJ1 APICE PRELIMINARY; PRT; 433 AA.
AC Q8MMJ1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Major royal jelly protein MRJP1 precursor (Major royal jelly protein
DE 1).
GN Name=MRJP1; Synonyms=mrjp1;
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Nurse heads;
RA Sittipraneed S., Imjongjirak C.;
RT "Molecular Cloning of Major Royal Jelly Protein (MRJP1) cDNA from Apis
RT cerana in Thailand.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Imjongjirak C., Klinbunga S., Sittipraneed S.;
RT "Cloning, Expression and Genomic Organization of Genes Encoding Major
RT Royal Jelly Protein 1 and 2 of the Honeybee (Apis cerana).";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF525776; AAM88281.2; -; mRNA.
DR EMBL; AY515688; AAS88556.1; -; Genomic_DNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW Signal.
FT SIGNAL 1 20 Potential.
SQ SEQUENCE 433 AA; 48969 MW; FEC24D6A4BC7BF2F CRC64;

Query Match 92.9%; Score 2023; DB 2; Length 433;
Best Local Similarity 91.3%; Pred. No. 1.1e-139;
Matches 377; Conservative 20; Mismatches 16; Indels 0; Gaps 0;
```

Qy	1	NILRGESLNKSLPILHEWKFFDYDPSGDERQDAILSGEYDYKNNYPSDDIQWHDKIFVT	60
Db	21	SILRGESLNKSLVLEHWKFFDYDPSGDERQDAILSGEYDYKNNYPSDDIQWHDKIFVT	80
Qy	61	MLRYNGVPSSLNVISKVGCGPILQYPDWSFAKYDDCDSGIVSASKLAIDKCDRLWVLD	120
Db	81	MLRYNGVPSSLNVISKVGCGPILQYPDWSFAKYDDCDSGIVSASKLAIDKCDRLWVLD	140
Qy	121	SGLVNNTQPMCSKLLTFDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNS	180
Db	141	SGLVNNTQPMCSKLLTFDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNS	200
Qy	181	DTMVYIADKEGGLIVYHNSDSEFHLRTSNTFYDPKFTKMTIDGESYTAQDGISGMA	240
Db	201	DTMVYIADKEGGLIVYHNSDSEFHLRTSNTFYDPKFTKMTIDGESYTAQDGISGMA	260
Qy	241	PMTNNLYSPVASTSLYYVNTQFRTSDYQNDIHVEGVQNILDTQSSAKVSKGVLPFF	300
Db	261	PMTNNLYSPVASTSLYYVNTQFRTSDYQNDIHVEGVQNILDTQSSAKVSKGVLPFF	320
Qy	301	GLVGDSALGCWNEHRLTLEHNRIRTVASQDETQMIASMKIKEAXPHVPIFDYINREYIL	360
Db	321	GLVGDSALGCWNEHRLTLEHNRIRTVASQDETQMIASMKIKEAXPHVPIFDYINREYIL	380
Qy	361	VLSNMKQKMNNDNFDDVFRIMNANVELILNTRCENPDNDRTPPKISIH	413
Db	381	VLSNMKQKMNNDNFDDVFRIMNANVELILNTRCENPDNDRTPPKISIH	433
RESULT 4			
ID	QSVLE2	APICC PRELIMINARY;	PRT; 433 AA.
AC	QSVLE2;		
DT	01-FEB-2005	(TrEMBLrel. 29, Created)	
DT	01-FEB-2005	(TrEMBLrel. 29, Last sequence update)	
DE	Major royal jelly protein MRJPI.		
OS	Apis cerana cerana (Oriental honeybee).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;		
OC	Apidae; Apis.		
OX	NCBI_TaxID=94128;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Head;		
RA	Songkun S., Shenglu C., Stefan A., Boxiong Z.;		
RT	"Molecular Cloning of MRJPI cDNA from Apis cerana cerana in China.";		
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY279539; AAQ16677.1; -; mRNA.		
DR	InterPro; IPR003534; Royaljelly.		
DR	Pfam; PF01022; MRJP; 1.		
DR	PRINTS; PR01366; ROYALJELLY.		
SQ	SEQUENCE 433 AA; 49045 MW; 86D6C115EF40B9B5 CRC64;		
Query Match			
Best Local Similarity 91.3%; Score 2020; DB 2; Length 433;			
Matches 377; Conservative 20; Mismatches 16; Indels 0; Gaps 0;			
Qy	1	NILRGESLNKSLPILHEWKFFDYDPSGDERQDAILSGEYDYKNNYPSDDIQWHDKIFVT	60
Db	21	SILRGESLNKSLVLEHWKFFDYDPSGDERQDAILSGEYDYKNNYPSDDIQWHDKIFVT	80
Qy	61	MLRYNGVPSSLNVISKVGCGPILQYPDWSFAKYDDCDSGIVSASKLAIDKCDRLWVLD	120
Db	81	MLRYNGVPSSLNVISKVGCGPILQYPDWSFAKYDDCDSGIVSASKLAIDKCDRLWVLD	140
Qy	121	SGLVNNTQPMCSKLLTFDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNS	180
Db	141	SGLVNNTQPMCSKLLTFDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNTNS	200
Qy	181	DTMVYIADKEGGLIVYHNSDSEFHLRTSNTFYDPKFTKMTIDGESYTAQDGISGMA	240

Db	201	DTMVYIADKEGGLIVYHNSDSEFHLRTSNTFYDPKFTKMTIDGESYTAQDGISGMA	260
Qy	241	PMTNNLYSPVASTSLYYVNTQFRTSDYQNDIHVEGVQNILDTQSSAKVSKGVLPFF	300
Db	261	PMTNNLYSPVASTSLYYVNTQFRTSDYQNDIHVEGVQNILDTQSSAKVSKGVLPFF	320
Qy	301	GLVGDSALGCWNEHRLTLEHNRIRTVASQDETQMIASMKIKEAXPHVPIFDYINREYIL	360
Db	321	GLVGDSALGCWNEHRLTLEHNRIRTVASQDETQMIASMKIKEAXPHVPIFDYINREYIL	380
Qy	361	VLSNMKQKMNNDNFDDVFRIMNANVELILNTRCENPDNDRTPPKISIH	413
Db	381	VLSNMKQKMNNDNFDDVFRIMNANVELILNTRCENPDNDRTPPKISIH	433
RESULT 5			
ID	Q6IMJ9	APIME PRELIMINARY;	PRT; 443 AA.
AC	Q6IMJ9;		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DE	Major royal jelly protein 7.		
GN	Name=MRJP7;		
OS	Apis mellifera (Honeybee).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;		
OC	Apidae; Apis.		
OX	NCBI_TaxID=7460;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	PubMed=15037093; DOI=10.1016/j.jinshys.2003.09.008;		
RT	Albert S., Klaudiny J.;		
RT	"The MRJP/YELLOW protein family of Apis mellifera: identification of		
RT	new members in the EST library.";		
RL	J. Insect Physiol. 50:51-59(2004).		
CC	-i- MISCCELLANEOUS: The sequence shown here is derived from an		
CC	EMBL/GenBank/DBJ third party annotation (TPA) entry.		
DR	EMBL; BK001420; DAA01512.1; -; mRNA.		
DR	Ensembl; ENSAPMG0000007331; Apis mellifera.		
DR	InterPro; IPR003534; Royaljelly.		
DR	Pfam; PF03022; MRJP; 1.		
DR	PRINTS; PR01366; ROYALJELLY.		
SQ	SEQUENCE 443 AA; 50541 MW; 8916272BA4DB421 CRC64;		
Query Match			
Best Local Similarity 66.8%; Score 1454.5; DB 2; Length 443;			
Matches 270; Conservative 66; Mismatches 63; Indels 13; Gaps 4;			
Qy	2	ILRGES---LNKSLPILHEWKFFDYDPSGDERQDAILSGEYDYKNNYPSDDIQWHDKIF	58
Db	19	ILRENSARNLKNLKNVHEWKFFDYDPSGDERQDAILSGEYDYKNNYPSDDIQWHDKIF	78
Qy	59	VTMLRYNGVPSSLNVISKVGCGPILQYPDWSFAKYDDCDSGIVSASKLAIDKCDRLWV	118
Db	79	VTMLRYNGVPSSLNVISKVGCGPILQYPDWSFAKYDDCDSGIVSASKLAIDKCDRLWV	138
Qy	119	LDSGLVNNTQPMCSKLLTFDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNT	178
Db	139	LDSGLVNNTQPMCSKLLTFDLTTSQLLKQVEIPHDVAVNATTGKRLSSSLAVQSLDCNT	195
Qy	179	NSDTMVYIADKEGGLIVYHNSDSEFHLRTSNTFYDPKFTKMTIDGESYTAQDGISGMA	238
Db	196	SVNTLVYIADKGDGLIVYHNSDSEFHLRTSNTFYDPKFTKMTIDGESYTAQDGISGMA	255
Qy	239	LSPMTNNLYSPVASTSLYYVNTQFRTSDYQNDIHVEGVQNILDTQSSAKVSKGVLP	298
Db	256	LSPMTNNLYSPVASTSLYYVNTQFRTSDYQNDIHVEGVQNILDTQSSAKVSKGVLP	315
Qy	299	PFGLVGDALGCWNEHRLTLEHNRIRTVASQDETQMIASMKIKEAXPHVPI--FDYINR	356
Db	316	PFGLVGDALGCWNEHRLTLEHNRIRTVASQDETQMIASMKIKEAXPHVPI--FDYINR	375

```
QY 357 EYLVLVSNKQKQVNVNDFNFDVNFPRIMANVNELILNTRC-----ENPDND 403
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 376 EYMLVLTNRMQKILNNDNFNFINFRILIGVSDLLNTRCTNFNTQNDSD 427

RESULT 6
MRJP2_APIME STANDARD; PRT; 452 AA.
AC 077061;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Major royal jelly protein 2 precursor (MRJP-2) (Bee-milk protein).
GN Name=MRJP2;
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
OX NCBI_TaxID=7460;
RN NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 18-30.
RP TISSUE=Head;
RC MEDLINE=99007754; PubMed=9791542; DOI=10.1007/s000180050229;
RA Schmitzova J., Klaudiny J., Albert S., Schroeder W., Schreckengost W.,
RA Hanes J., Judova J., Simuth J.;
RT "A family of major royal jelly proteins of the honeybee Apis mellifera
RT L.";
RL Cell. Mol. Life Sci. 54:1020-1030(1998).
CC -I- FUNCTION: May play an important role in honeybee nutrition. It is
CC found in the royal jelly which is the food of the queen honey bee
CC larvae. The royal jelly determines the development of the young
CC larvae and is responsible for the high reproductive ability of the
CC honeybee queen.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Found in the hypopharyngeal glands.
CC -I- DEVELOPMENTAL STAGE: Produced in the cephalic glands of the nurse
CC honeybee.
CC -I- SIMILARITY: Belongs to the major royal jelly protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL; AF000632; AAC61894.1; -; mRNA.
DR Ensembl; ENSAPMG00000004182; Apis mellifera.
DR InterPro; IPR003534; Royaljelly.
DR PANTHER; PTHR10009; Royaljelly; 1.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW Direct protein sequencing; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 452 Major royal jelly protein 2.
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 452 AA; 51074 MW; 25E5B621288FE189 CRC64;

Query Match 66.28; Score 1441; DB 1; Length 452;
Best Local Similarity 67.88; Pred. No. 5.1e-97;
Matches 270; Conservative 57; Mismatches 67; Indels 4; Gaps 2;

QY 7 SLNKSPLILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSPDIDQWHDKIFVTMLRYNG 66
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 27 NLEKSLNVHIEWKYDYDFGSEERRQAAIQSGEYDHTKNYPFDVQWDRDXTFTILRYDG 86

QY 67 VPSSLNVISKVGGGGLLPQYPDWSFAYKDDCSGIVSASKLAIDKCDRLWLVDGLVNN 126
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 87 VPSTLNVISGKTGGKGLLPQYPDWSFAEFKDCSKIVSAFKIAIDKFDRLWLVDGLVNR 146

QY 127 TOPMCSPKLLTFTLTTSOLLKQVEIPHDAVNATTGKGRSLSSLAQSLDCNTNSDTWYI 186
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 147 TVPVCAPKLHVFLDKTNSHLKQIEIPHDAVNATTGKGLVSLAVQAIDL---ANTLVYM 203
```

```
QY 187 ADEKGGGLIVYHNSSDSSFRLTSNTFYDPKFTYKMTIDGESYTAQDGISGMALSPMTNNL 246
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 204 ADHKGDALIVYQNAADDSFRLTSNTFYDPRYAKMTIDGESFTLKNGICGMALSPVTNNL 263

QY 247 YTSVPVASTSIYYUNTEQFRTSDYQONDIIHYEGVQNILDTQSSAKVYKSGVLPFGVLGDS 306
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 264 YYSPLASHGLIYYVNTAPFMKQSGFGENNVQVQSGEDILNTQSLAKAVSKNGVLPFGVLGNS 323

QY 307 ALGCWNEHRTLERHNIRTVQAQSDETLQMIASMKIKEAPHPVIFDFYINREYILVLSNKM 366
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 324 AVGCWNEHQSLOQNLEMAQNDRITLQMIAGMKIKEELPHFVGSNPKPVKDEYMLVLSNRM 383

QY 367 QKVVNDFNFDVNFPRIMANVNELILNTRC--ENPDND 403
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 384 QKIVNDDFNFDVNFRIILGANVKELIRNTHCVNNNQND 421

RESULT 7
Q8MMJ0_APICE PRELIMINARY; PRT; 463 AA.
AC Q8MMJ0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Major royal jelly protein MRJP2 precursor.
GN Name=MRJP2;
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apoidea; Apis.
OX NCBI_TaxID=7461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Nurse heads;
RA Sittipraneeed S., Imjongjirak C.;
RT "Molecular Cloning of Major Royal Jelly Protein (MRJP2) cDNA from Apis
RT cerana in Thailand.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF525777; AAM88282.2; -; mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW Signal.
FT SIGNAL 1 17
FT SEQUENCE 463 AA; 52490 MW; 29D92E3749B15992 CRC64;

Query Match 64.88; Score 1411; DB 2; Length 463;
Best Local Similarity 66.38; Pred. No. 8.2e-95;
Matches 264; Conservative 60; Mismatches 70; Indels 4; Gaps 2;

QY 6 ESLNKSPLILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSPDIDQWHDKIFVTMLRYN 65
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 26 KULESLNVHIEWKYDYDFGSEERRQAAIQSGEYDHTKNYPFDVQWHDKFTVILKYD 85

QY 66 GVPSSLNVISKVGGGGLLPQYPDWSFAYKDDCSGIVSASKLAIDKCDRLWLVDGLVNN 125
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 86 GVPSTLNMISNKTGGKGLLPQYPDWSAENKDCSGIVSAFKIAIDKFDRLWLVDGLVNN 145

QY 126 NTPMCSPKLLTFTLTTSOLLKQVEIPHDAVNATTGKGRSLSSLAQSLDCNTNSDTWYI 185
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 146 RTEPICAPKLHVFLDKTNSHLKQIEIPHDAVNATTGKGLVSLVQAMD---PMNTLVY 202

QY 186 IADEKGGGLIVYHNSSDSSFRLTSNTFYDPRYAKMTIDGESYTAQDGISGMALSPMTNN 245
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 203 IADHKDALIVYQNSDSSFRLTSNTFYDPRYAKMTIDGESFTLKNGICGMALSPVTNN 262

QY 246 LYTSVPVASTSIYYUNTEQFRTSDY--QONDIHYEGVQNILDTQSSAKVYKSGVLPFGVLG 304
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 263 LYTSPLASHGLIYYVNTPEFMKQSGFGENNVQVQSGEDTLNTQSLAKAVSKGVLFGVLG 322

QY 305 DSALGCWNEHRTLERHNIRTVQAQSDETLQMIASMKIKEAPHPVIFDFYINREYILVLSN 364
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 364
```


Db	323	NSALGCLNEHQLORENLELVAQNEKTLQMIAGMKIKEELPHFVGSNKPVKDEYMLVLSN	382
Qy	365	KMQKVVNNDFNFDVNFPRIMANVNNELILNTRCENPDN	402
Db	383	KMQKVVNNDFNFDVNFRIILGANVKELMRNTHCANFNN	420
RESULT 8			
Q50H66	APICE		
ID	Q50H66	APICE PRELIMINARY;	PRT; 463 AA.
AC	Q50H66;		
DT	13-SEP-2005	(T-EMBLrel. 31, Created)	
DT	13-SEP-2005	(T-EMBLrel. 31, Last sequence update)	
DT	13-SEP-2005	(T-EMBLrel. 31, Last annotation update)	
DE	Major royal jelly protein 2.		
GN	Name=mrjpl;		
OS	Apis cerana (Indian honeybee).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;		
OC	Apidae; Apis.		
OX	NCBI_TaxID=7461;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Imjongjirak C., Klinbunga S., Sittipraneed S.;		
RT	"Cloning, Expression and Genomic Organization of Genes Encoding Major		
RT	Royal Jelly Protein 1 and 2 of the Honeybee (Apis cerana).";		
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY515689; AAS88557.1; -; Genomic DNA.		
SQ	SEQUENCE 463 AA; 52462 MW; 930C91C8CC595935 CRC64;		
Query Match 64.8%; Score 1411; DB 2; Length 463;			
Best Local Similarity 66.3%; Pred. No. 8.2e-95;			
Matches 264; Conservative 60; Mismatches 70; Indels 4; Gaps 2;			
Qy	6	ESLNKSLPILHEWKFFDYDFGSDERRQDAILSGEYDYKNYPSPSIDQWHDKIFVTMLRYN	65
Db	26	KNLESLNVLHWEKYYIDYDFGSEERRQAAIQSGEYDHTKNYPDFVDQWHDKTFVILKYD	85
Qy	66	GVPSLSNVISKVGDGGLLPQYPDWSFAKYDDCSGIVSASKLAIDKCDRLWLDSGLVN	125
Db	86	GVPSLTNLMISNKIKGGKRLLPYPDWSWAENKDCSGIVSAFKIAIDKFDRLWLDSGLIN	145
Qy	126	NTQPMCSKPLTFLDITTSQLLKQVEIPHDVAVNATTGKRLSSLAQVSLCQNTNSDTMYY	185
Db	146	RTEPICAPKLHVFDLKNTHKQLKQIEIPHDIAVNATTGKGLVSLVQAMD---PMNTLVY	202
Qy	186	IADKGEGLIVYHNSDDSFHRLTNTFDYDPKFTKMTIDGESYTAQDGISGMALSPMTNN	245
Db	203	IADHKGDALIVYQNSDDSFHRTSNTFDYDPYAKMTINGESFTLKNGICGMALSPVTNN	262
Qy	246	LYSPVASTSLYYVNTPEQFTSDY-QQNDIHYEGVQNILDTQSSAKVSVSGVLFFGLVG	304
Db	263	LYSPSLASHGLYYVNTPEPFMKSQFGDNNVQYEGSQDTLNTQSLAKAVSKDGLVFLVGLG	322
Qy	305	DSALGCWNEHRTLEHNIPTVAQSDETLOMTASKIKEAPHPVIFDRIYNREYILVLSN	364
Db	323	NSALGCLNEHQLORENLELVAQNEKTLQMIAGMKIKEELPHFVGSNKPVKDEYMLVLSN	382
RESULT 9			
Q5VK55	APICC		
ID	Q5VK55	APICC PRELIMINARY;	PRT; 468 AA.
AC	Q5VK55;		
DT	01-FEB-2005	(TrEMBLrel. 29, Created)	
DT	01-FEB-2005	(TrEMBLrel. 29, Last sequence update)	
DT	01-FEB-2005	(TrEMBLrel. 29, Last annotation update)	
DE	Major royal jelly protein MRJP2.		
OS	Apis cerana cerana (Oriental honeybee).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		

OC	Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;		
OC	Apidae; Apis.		
OX	NCBI_TaxID=94128;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Su S., Chen S., Albert S.;		
RT	"Molecular cloning of MRJP2 cDNA from Apis cerana cerana in China.";		
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY392758; AAR83083.1; -; mRNA.		
DR	InterPro; IPR003534; Royaljelly.		
DR	Pfam; PF03022; MRJP; 1.		
DR	PRINTS; PR01366; ROYALJELLY.		
SQ	SEQUENCE 468 AA; 53060 MW; 5B2A6AEF4C530C84 CRC64;		
Query Match 64.8%; Score 1411; DB 2; Length 468;			
Best Local Similarity 66.3%; Pred. No. 8.4e-95;			
Matches 264; Conservative 60; Mismatches 70; Indels 4; Gaps 2;			
Qy	6	ESLNKSLPILHEWKFFDYDFGSDERRQDAILSGEYDYKNYPSPSIDQWHDKIFVTMLRYN	65
Db	26	KNLESLNVLHWEKYYIDYDFGSEERRQAAIQSGEYDHTKNYPDFVDQWHDKTFVILKYD	85
Qy	66	GVPSLSNVISKVGDGGLLPQYPDWSFAKYDDCSGIVSASKLAIDKCDRLWLDSGLVN	125
Db	86	GVPSLTNLMISNKIKGGKRLLPYPDWSWAENKDCSGIVSAFKIAIDKFDRLWLDSGLIN	145
Qy	126	NTQPMCSKPLTFLDITTSQLLKQVEIPHDVAVNATTGKRLSSLAQVSLCQNTNSDTMYY	185
Db	146	RTEPICAPKLHVFDLKNTHKQLKQIEIPHDIAVNATTGKGLVSLVQAMD---PMNTLVY	202
Qy	186	IADKGEGLIVYHNSDDSFHRLTNTFDYDPKFTKMTIDGESYTAQDGISGMALSPMTNN	245
Db	203	IADHKGDALIVYQNSDDSFHRTSNTFDYDPYAKMTINGESFTLKNGICGMALSPVTNN	262
Qy	246	LYSPVASTSLYYVNTPEQFTSDY-QQNDIHYEGVQNILDTQSSAKVSVSGVLFFGLVG	304
Db	263	LYSPSLASHGLYYVNTPEPFMKSQFGDNNVQYEGSQDTLNTQSLAKAVSKDGLVFLVGLG	322
Qy	305	DSALGCWNEHRTLEHNIPTVAQSDETLOMTASKIKEAPHPVIFDRIYNREYILVLSN	364
Db	323	NSALGCLNEHQLORENLELVAQNEKTLQMIAGMKIKEELPHFVGSNKPVKDEYMLVLSN	382
Qy	365	KMQKVVNNDFNFDVNFPRIMANVNNELILNTRCENPDN	402
Db	383	KMQKVVNNDFNFDVNFRIILGANVKELMRNTHCANFNN	420
RESULT 10			
MRJP3	APIME		
ID	MRJP3	APIME STANDARD;	PRT; 544 AA.
AC	Q17060;		
DT	28-FEB-2003	(Rel. 41, Created)	
DT	28-FEB-2003	(Rel. 41, Last sequence update)	
DT	10-MAY-2005	(Rel. 47, Last annotation update)	
DE	Major royal jelly protein 3 precursor (MRJP-3) (Bee-milk protein)		
DE	(Royal jelly protein RJP57-1).		
GN	Name=MRJP3;		
OS	Apis mellifera (Honeybee).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;		
OC	Apidae; Apis.		
OX	NCBI_TaxID=7460;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Head;		
RA	Klaudiny J., Hanes J., Kulifajova J., Albert S., Simuth J.;		
RT	"Molecular cloning of two cDNAs from the head of the nurse honey bee		
RT	(Apis mellifera L.) for coding related proteins of royal jelly.";		
RL	J. Apicultural Res. 33:105-111 (1994).		
RN	[2]		
RP	SEQUENCE REVISION TO THE C-TERMINUS.		
RA	Albert S., Klaudiny J., Simuth J.;		
RT	"Newly discovered features of the updated sequence of royal jelly		

RT protein_RJP571; longer repetitive region on C-terminus and homology to
 RT Drosophila melanogaster yellow protein.";
 RL J. Apicultural Res. 35:63-68(1996).
 RN [3]
 RN NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 21-36.
 RC TISSUE=Head;
 RX MEDLINE=99007754; PubMed=9791542; DOI=10.1007/s000180050229;
 RA Schmitzova J., Klaudiny J., Albert S., Schroeder W., Schreckengost W.,
 RA Hanes J., Judova J., Simuth J.;
 RT "A family of major royal jelly proteins of the honeybee Apis mellifera
 L.";
 RL Cell. Mol. Life Sci. 54:1020-1030(1998).
 RN [4]
 RN NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE OF 45-59; 70-77;
 RP 106-120; 214-224 AND 243-253.
 RC TISSUE=Hypopharyngeal gland;
 RX MEDLINE=98055707; PubMed=9395329;
 RA Chaishi K., Natori S., Kubo T.;
 RT "Change in the mode of gene expression of the hypopharyngeal gland
 RT cells with an age-dependent role change of the worker honeybee Apis
 mellifera L.";
 RL Eur. J. Biochem. 249:797-802(1997).
 CC -!- FUNCTION: May play an important role in honeybee nutrition. It is
 CC found in the royal jelly which is the food of the queen honey bee
 CC larva. The royal jelly determines the development of the young
 CC larvae and is responsible for the high reproductive ability of the
 CC honeybee queen.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Hypopharyngeal glands of nurse honey bees.
 CC -!- DEVELOPMENTAL STAGE: Produced by the cephalic glandular system of
 CC the nurse honey bee.
 CC -!- SIMILARITY: Belongs to the major royal jelly protein family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; Z26318; CAA81227.1; -; mRNA.
 DR Ensembl; ENSAPMG0000007331; Apis mellifera.
 DR InterPro; IPR003534; Royaljelly.
 DR PANTHER; PTHR10009; Royaljelly.
 DR Pfam; PF03022; MRJP, 1.
 DR PRINTS; PR01366; ROYALJELLY.
 KW Direct protein sequencing; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 544 Major royal jelly protein 3.
 FT REPEAT 424 428 1.
 FT REPEAT 429 433 2.
 FT REPEAT 434 438 3.
 FT REPEAT 439 443 4.
 FT REPEAT 444 448 5.
 FT REPEAT 449 453 6.
 FT REPEAT 454 458 7.
 FT REPEAT 459 463 8.
 FT REPEAT 464 468 9.
 FT REPEAT 469 473 10.
 FT REPEAT 474 478 11.
 FT REPEAT 479 483 12.
 FT REPEAT 484 488 13.
 FT REPEAT 489 493 14.
 FT REPEAT 494 498 15.
 FT REPEAT 499 503 16.
 FT REPEAT 504 508 17.
 FT REPEAT 509 513 18.
 FT REPEAT 514 518 19.
 FT REPEAT 519 523 20.
 FT REGION 424 523 20 x 5 AA tandem repeats of [NKR]-Q-N-
 FT [AGD]-[DNG].
 FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).
 FT SEQUENCE 544 AA; 61662 MW; 4C8FFFCBA2759F52 CRC64;

Query Match 64.6%; Score 1406.5; DB 1; Length 544;
 Best Local Similarity 64.8%; Pred. No. 2.2e-94;
 Matches 263; Conservative 62; Mismatches 68; Indels 13; Gaps 2;
 QY 7 SLNKLSPILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSDIDQWHDKIFVTMLRYNG 66
 DB 32 NLAHSMKVIYEWKHDIDFGSDERRDAALKSSEFDTKYPFPDVRWRDKTFTTIERNG 91
 QY 67 VPSLNVISKVGDGGLLPQPDWSFAKYDCSGIVSASKLAIDKCDRLWLDLSGLVNN 126
 DB 92 VPSLNVVTKKGKGGPILLRPYDWSFAKYDCSGIVSFAKIAVDKFDRLWLDLSGLVNN 151
 QY 127 TQPMCSPKLLTFDLTTSQLLKQVEIPHDVAVNATTKGRLSSLAQSLDCNTNSDTMVI 186
 DB 152 NQPMCSPKLLTFLDKTSKLVQVEIPHNIAVNATTGMGELVSLAQDAID---RTNTMVI 208
 QY 187 ADEKGGELJLVHNSDDSPHRLTSNTFDYDPKFTMTIDGESYTAODGISGMALSPMTNNL 246
 DB 209 ADEKGGELIMYQNSDDSPHRLTSNTFDYDPKFTMTIDGESYTAODGISGMALSPMTNNL 268
 QY 247 YVSPVASTSLYYVNTQFRTSDYQQNDIHYEGVQNILDTQSSAKVSVKSGVLFGLVGDS 306
 DB 269 YVSPVASTSLYYVNTQFRTSDYQQNDIHYEGVQNILDTQSSAKVSVKSGVLFGLVGDS 328
 QY 307 ALGCWNEHRTLERNIRTVQASDETLQMIASMKIEXAPHPVPIFDRIYINREYILVLSNM 366
 DB 329 GIACVNEHQVLRQESFDVVAQNEETLQMIASMKIEXAPHPVPIFDRIYINREYILVLSNM 388
 QY 367 QKWNNDNFDDVNFPRIMNAVNNELILNTRC-----ENPDN 402
 DB 389 QKIINDDNFNDVNFRLGANNVDDLMNTRCGRYHNQAGNQADN 434
 RESULT 11
 Q6W3E3 APIME
 ID Q6W3E3 APIME PRELIMINARY; PRT; 437 AA.
 AC Q6W3E3;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Major royal jelly protein MRJP6.
 OS Apis mellifera (Honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Apidae; Apis.
 OX NCBI_TaxID=7460;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15037093; DOI=10.1016/j.jinphys.2003.09.008;
 RA Albert S., Klaudiny J.;
 RT "The MRJP/YELLOW protein family of Apis mellifera: identification of
 RT new members in the EST library.";
 RL J. Insect Physiol. 50:51-59(2004).
 DR EMBL; AY133893; AAQ82184.1; -; mRNA.
 DR Ensembl; ENSAPMG00000007331; Apis mellifera.
 DR InterPro; IPR003534; Royaljelly.
 DR Pfam; PF03022; MRJP, 1.
 DR PRINTS; PR01366; ROYALJELLY.
 DR SEQUENCE 437 AA; 49786 MW; 1B654BB7A7F0B56D CRC64;
 Query Match 64.3%; Score 1401; DB 2; Length 437;
 Best Local Similarity 63.3%; Pred. No. 4.1e-94;
 Matches 260; Conservative 69; Mismatches 76; Indels 6; Gaps 2;
 QY 6 ESLNKLSPILHEWKFFDYDFGSDERRQDAILSGEYDYKNNYPSDIDQWHDKIFVTMLRYN 65
 DB 29 KMLEHSMNVHEWKYIDYDFGSDERRQDAILSGEYDYKNNYPSDIDQWHDKIFVTMLRYN 88
 QY 66 GVPSSLNVTSKKVGDDGGLLPQPDWSFAKYDCSGIVSASKLAIDKCDRLWLDLSGLV 125
 DB 89 GVPSSLNVTSEKINGGCLLPQPDWSWANYKDCSGIVSAYKIAIDKFDRLWLDLSGLIN 148
 QY 126 NTQPMCSPKLLTFLDTTSQLLKQVEIPHDVAVNATTKGRLSSLAQSLDCNTNSDTMVI 185

Db 149 NIOQMCSKLLADLNTSKLLAQIEPHNIAVNASGMPVSLVQAMD---PMNTTVY 205
QY 186 IADKEGGLIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALSPMTNN 245
Db 206 IADDRGDALIIYQNSDDSFHRLTSKTFDNDLRYSELAVAGESFTVHDGIFGMALSPVTNN 265
QY 246 LYTSPVASTLYYVNTTEQRTSDYQONDIIHYEGVONILDTQSSAKVSKGVLFPGLVGD 305
Db 266 LYTSPLTSLHYVNMPEPFMKSYEENNIYEGIQDIFNTQSSAKVSKGVLFPGLVNN 325
QY 306 SALGCWNEHRTLRHNI RTVAQSDTLQMIASMKI KEAXPHVPIDRYINREYILVLSNK 365
Db 326 SALGCWNEHQPLOQRQNDWVAQNEKTLOMIISVKIIQNLAISGRMNRHKNKYMALSNR 385
QY 366 MQKVVNDFNFDVFRIMANVNELILNTRC---ENPDNDRTFPFKISIH 413
Db 386 MQKIVNDFNFDVFRILGANVNLIKNTRCAKSNQNNQNKYKQNAHL 436

RESULT 12
Q6QN15 APICE
ID Q6QN15 APICE PRELIMINARY; PRT; 579 AA.
AC Q6QN15;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Major royal jelly protein MRJP5 precursor.
GN Name=MRJP5;
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypopharyngeal gland;
RA Sittipraneed S.; Cenphakdee K.;
RT "Molecular Cloning of Major Royal Jelly Protein (MRJP5) cDNA from Apis cerana in Thailand."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY532369; AAS21320.1; -: mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 2.
DR PRINTS; PRO1366; ROYALJELLY.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 1 20 Potential.
Query Match 1 20 Potential.
Best Local Similarity 579 AA; 68289 MW; 8218A56B12024F2 CRC64;
Matches 265; Conservative 63; Mismatches 61; Indels 158; Gaps 5;

QY 7 SLNKLPLILHEWKFFDYDFGSDERRQDAILSGEYDYKKNYPSPDIDQWHDKIFVTMLRYNG 66
Db 30 NLANSMNVIIHEWKYLDYDFGSDERKQAAIQSGEYDHTKNYPFDVDRWHDMTFVTLRYKG 89
QY 67 VPSSLNVISSKVGDDGGLLPQYPDWSFAKYDDCSGIVSASKLAIDKCDRLWVLSGLVNN 126
Db 90 VPSSLNVISSKIGNGGGLLPQYPDWSWANYKDCSGIVSAYKIAIDKDFRLWVLSGIINN 149
QY 127 TQPCSKPLTFDITTSQLLKQVEI PHDVAVNATTGKRLSSLAQSLDCNTNSDTWYI 186
Db 150 TQPCSKPLHFDLNTSQIKQVMMPHDIAINATTGKGLNVLVQAMD---PMNTLVYM 206
QY 187 ADEKGLIIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALSPMTNNL 246
Db 207 ADNKGDAIIVYQNSDDSFHRLTSNTFDYDPKIIYKMAAGESFTIQDGI FGMALSPMTNNL 266
QY 247 YISPVASTLYYVNTTEQRTSDYQONDIIHYEGVONILDTQSSAKVSKGVLFPGLVGD 306
Db 267 YISPLASRLSYVNTKPFMKSYQGTNNVQHEGVQDIFNTQSIKIMSKNGVLFPGLMNS 326

QY 307 ALGCWNEHRTLRHNI RTVAQSDTLQMIASMKI KEAXPHVPIDRYINREYILVLSNK 348
Db 327 ALGCWNEHQPLOQRQNDWVAQNEETLTQTVVAKMM---HLPOSNRMRHMRMSNMNRMD 382
QY 349 ---IFDR--- 352
Db 383 RMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMD 442
QY 353 ---YINR--- 356
Db 443 KMVMRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMD 502
QY 357 ---EYILVLSNKQKQKVVNDFNFDVFRIMANVNELILNTRC---ENPDNDRTFPFKISIH 395
Db 503 MHRMGRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMDRMD 562
QY 396 RCENPDN 402
Db 563 RCANSNN 569

RESULT 13
Q5VK56 APICC
ID Q5VK56 APICC PRELIMINARY; PRT; 598 AA.
AC Q5VK56;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Major royal jelly protein MRJP5.
OS Apis cerana cerana (Oriental honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=94128;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Su S.; Chen S.; Albert S.; Zhong B.;
RT "Molecular cloning of MRJP5 cDNA from Apis cerana."
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY392757; AAR83082.1; -: mRNA.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 2.
DR PRINTS; PRO1366; ROYALJELLY.
SQ SEQUENCE 598 AA; 70522 MW; DD931CA92F433DF2 CRC64;

Query Match 61.7%; Score 1343.5; DB 2; Length 598;
Best Local Similarity 46.6%; Pred. No. 1e-89;
Matches 264; Conservative 64; Mismatches 61; Indels 177; Gaps 5;
QY 7 SLNKLPLILHEWKFFDYDFGSDERRQDAILSGEYDYKKNYPSPDIDQWHDKIFVTMLRYNG 66
Db 30 NLANSMNVIIHEWKYLDYDFGSDERKQAAIQSGEYDHTKNYPFDVDRWHDMTFVTLRYKG 89
QY 67 VPSSLNVISSKVGDDGGLLPQYPDWSFAKYDDCSGIVSASKLAIDKCDRLWVLSGLVNN 126
Db 90 VPSSLNVISSKIGNGGGLLPQYPDWSWANYKDCSGIVSAYKIAIDKDFRLWVLSGIINN 149
QY 127 TQPCSKPLTFDITTSQLLKQVEI PHDVAVNATTGKRLSSLAQSLDCNTNSDTWYI 186
Db 150 TQPCSKPLHFDLNTSQIKQVMMPHDIAINATTGKGLNVLVQAMD---PMNTLVYM 206
QY 187 ADEKGLIIVYHNSDDSFHRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALSPMTNNL 246
Db 207 ADNKGDAIIVYQNSDDSFHRLTSNTFDYDPKIIYKMAAGESFTIQDGI FGMALSPMTNNL 266
QY 247 YISPVASTLYYVNTTEQRTSDYQONDIIHYEGVONILDTQSSAKVSKGVLFPGLVGD 306
Db 267 YISPLASRLSYVNTKPFMKSYQGTNNVQHEGVQDIFNTQSIKIMSKNGVLFPGLMNS 326
QY 307 ALGCWNEHRTLRHNI RTVAQSDTLQMIASMKI KEAXPHVPIDRYINREYILVLSNK 348
Db 327 ALGCWNEHQPLOQRQNDWVAQNEETLTQTVVAKMM---HLPOSNRMRHMRHMRMSNMNRMD 382

File Page Blank (usp.c)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:09:24 ; Search time 44.6142 Seconds
(without alignments)
765.341 Million cell updates/sec

Title: US-10-525-567-4

Perfect score: 2178

Sequence: 1 NIIRGSLNKLPIHWEKF.....NTRCENPDNRTFFKLSIHL 413

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5 COMB pep.*

2: /cgn2_6/ptodata/1/iaa/6 COMB pep.*

3: /cgn2_6/ptodata/1/iaa/H COMB pep.*

4: /cgn2_6/ptodata/1/iaa/PTCUS COMB pep.*

5: /cgn2_6/ptodata/1/iaa/RE COMB pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1 pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	233	10.7	162	2	US-09-270-767-33773
2	233	10.7	162	2	US-09-270-767-48990
3	126	5.8	163	2	US-09-270-767-32344
4	126	5.8	163	2	US-09-270-767-47561
5	116.5	5.3	161	2	US-09-270-767-43507
6	108.5	5.0	1427	2	US-09-902-540-10612
7	105	4.8	159	2	US-09-270-767-32059
8	105	4.8	159	2	US-09-270-767-47276
9	104	4.8	956	2	US-09-134-001C-4452
10	103	4.7	3852	2	US-10-025-225-4
11	103	4.7	4585	2	US-10-025-225-6
12	103	4.7	4588	2	US-10-025-225-8
13	103	4.7	4589	2	US-10-025-225-2
14	102	4.7	471	2	US-09-134-001C-3150
15	101.5	4.7	789	2	US-09-134-000C-4939
16	100.5	4.6	2308	1	US-08-015-973-1
17	100.5	4.6	2308	1	US-08-448-164-1
18	100.5	4.6	2308	2	US-08-081-929-2
19	100.5	4.6	2308	2	US-10-000-954-2
20	100.5	4.6	2314	2	US-09-816-703A-2
21	99	4.5	823	2	US-10-101-464A-923
22	98.5	4.5	461	2	US-09-252-991A-29720
23	98.5	4.5	970	1	US-08-673-789-7
24	98.5	4.5	1007	2	US-08-961-083-216
25	98.5	4.5	1007	2	US-09-536-784-216
26	98.5	4.5	1007	2	US-09-765-271-216
27	98.5	4.5	1007	2	US-09-765-272A-216

28	98.5	4.5	2026	2	US-09-487-558B-86	Sequence 86, Appl
29	97.5	4.5	371	2	US-09-991-181-171	Sequence 171, App
30	97.5	4.5	371	2	US-09-990-444-171	Sequence 171, App
31	97.5	4.5	371	2	US-09-997-333-171	Sequence 171, App
32	97.5	4.5	371	2	US-09-992-598-171	Sequence 171, App
33	97.5	4.5	392	2	US-09-248-796A-16779	Sequence 16779, A
34	97.5	4.5	881	2	US-09-248-796A-18627	Sequence 18627, A
35	97.5	4.5	1608	2	US-09-568-407-1	Sequence 1, Appli
36	96	4.4	432	2	US-09-270-767-46441	Sequence 46441, A
37	96	4.4	650	2	US-09-487-558B-430	Sequence 430, App
38	95.5	4.4	356	2	US-09-270-767-43404	Sequence 43404, A
39	95	4.4	576	2	US-09-248-796A-20509	Sequence 20509, A
40	95	4.4	781	2	US-09-538-092-363	Sequence 363, App
41	94.5	4.3	194	2	US-09-673-395A-253	Sequence 253, App
42	94.5	4.3	669	2	US-09-134-000C-6185	Sequence 6185, Ap
43	94.5	4.3	872	1	US-08-387-942C-5	Sequence 5, Appli
44	94.5	4.3	2391	1	US-08-446-855A-2	Sequence 2, Appli
45	94.5	4.3	2391	2	US-09-150-741-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-270-767-33773

; Sequence 33773, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 33773

; LENGTH: 162

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; US-09-270-767-33773

Query Match 10.7%; Score 233; DB 2; Length 162;

Best Local Similarity 42.1%; Pred. No. 8.5e-15;

Matches 48; Conservative 25; Mismatches 29; Indels 12; Gaps 5;

Qy	43	KNTVPSIDQWHDKIFVTMLRY-NGVSSLNVI	---SKKVGCGGLLPQYDWSF---AK 95
Db	11	KNNLPLGIDVHNNRLFVTTPRKNGVPASLTLPFSK--GVKGPALKPYNWEAHGNPN 68	
Qy	96	YDCSGIVSASKLAIDKCDRLWLDGLVN---NTQPMCSPKLTLTDTTSQLL 146	
Db	69	NPDCSKLSVYRTAVDRCDRLWLDGIIVNATINLNCICPKIVYVDLKSDELI 122	

RESULT 2

US-09-270-767-48990

; Sequence 48990, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 48990

; LENGTH: 162

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; US-09-270-767-48990

Query Match 10.7%; Score 233; DB 2; Length 162;

Query Match 4.8%; Score 105; DB 2; Length 159;
Best Local Similarity 23.3%; Pred. No. 0.034;

	Query Match	4.8%; Score 104; DB 2; Length 956;
	Best Local Similarity	19.4%; Pred. No. 0.82; Indels 182; Gaps 23
	Matches	99; Conservative 69; Mismatches 159;
Qy	56 KIFVTMLRYNGVPSSLNVISKKVGDGGPLLPYPDWSFAKYDDCSGIWASAKLAID----	111
Db	101 KMFEELKLENVEVKLTNIEGFHAG-----YIFEHHHTSFICGSSNLSTNAKL	151
Qy	112 -----KCRLW-----VLDSGLV	124
Db	152 NYEHNFLSTHKGDLVNNIKHKFDELWDSSFSLTNEWINKEYKOSFEQTLOKVPDNIVV	211
Qy	125 NNTQ---PMCSGPKLTLFDLTTSQLKQVEIPHDVA-----VNAT-TGKRGLSSIAVOQLD	175
Db	212 QNSEIKKFENESKLKPNIHQEAHLKSLESLRNVGGEKGLIIISATGTGKTILCALDVRAV-	270
Qy	176 CNTNSDTMWVIADSKG-----EGLIYVHNSSDS-FHRLTSNTFYDPDKTKMTIDGES	227
Db	271 ---SPDKFLFIHVNEGILNRALBSFKKVPYDESDFGLLTGKRDHDAKFLFATIQLS	327
Qy	228 -----YTQDGSGHALSP-MTNNLYYSPA	252
Db	328 KKENVKFNNSNHDFIYVFDEAHRTAASSYQKIFYNFKNPFLMGTMATPERTDELINIFELF	387
Qy	253 STSL-YVYNTSQ-----PRSTDYOQNDIHVEGVNQILDTQSAAKV---VSKSG	296
Db	388 NYNIAYEIRLOEALESNILCPHFVGVDYIQNEMSQEDAFNLKYLASNERVEHIKKTN	447
Qy	297 VLFGLGVDSALG-----CWNEHRTLBRHNRTV-----AQSDETLQMIAHWK	339
Db	448 --YVGYSDDVVKGLIFVSSRGEAYQLANQLSKRGISSVGLTGTKDSIAYRTETIQ-----Q	500
Qy	340 IKEAXPH----VPIDRVYNRE-----YILVSNMQGMVNDFNPDV	379
Db	501 IKEGSINYIIVDLPNEGIDIPEINOVVMRLPTKSSIIIFIQOLGRGLRKSTNKCF-VTVI	559

```

Qy 380 NFRIMNANVELI-----LNTRCENPDNDR 404
   :| | | | | | | | | | | | | | | |
Db 560 DF-IGNYKTYMPIALSGNKSQKNQYR 587

RESULT 10
US-10-025-225-4
; Sequence 4, Application US/10025225
; Patent No. 6852844
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Miracar
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6852844el Human Protocadherin Proteins and Polynucleotides Er
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0285-USA
; CURRENT APPLICATION NUMBER: US/10/025,225
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/257,257
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3852
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-025-225-4

Query Match 4.7%; Score 103; DB 2; Length 3852;
Best Local Similarity 19.4%; Pred. No. 10;
Matches 79; Conservative 78; Mismatches 162; Indels 88; Gaps 19;

Qy 62 LRYNGVPSSLNVISKVGDGGLLPYPYDMSFAKYDDCSGIVSASKLAIDKCDR----- 115
Db 2063 LRVARVVVRVNI--EDINDNSPVFVGUPYAAVQVDAEPGLTIYQVTAIDK-DKGPNGEV 2119

Qy 116 LWVL-----DSGLVNTNTPMCGSP-----KLTFTDLTTSQLLKQVEIHPDVA 156
Db 2120 TYVLQDDYGHFEINPNSGNVLKEAFNDSLNIIEYGVGTILAKDGGKPSLTSVELPTIV 2179

Qy 157 VNATTGKRLSSLAQSLDCNTNSDTM-VYIADEKGEGLIVYHNSDDSFRLITSNFTDYD 215
Db 2180 NKAMPVDFKPFYATSVNEDIRMTNPILLSINATSPGQGIIYIIDGPPFKQF---NIDFD 2236

Qy 216 PKFTMT--IDGE-----SYTAQDGGISG-----MALSPMTNN--LYYSPVASTSL 256
Db 2237 TGVLUKVVSPDLDEYVTSYKUTIRASDALTGARAEVTVDLLVNDVNDNPPIDPQTYNTTL 2296

Qy 257 ---YYVNTQFRT----SDYQQND-IHYEGVQNILDTQSSAKVVSXGVLFFGLVGDSDL 308
Db 2297 SEASLICTPVLQVVSIDADSNNKWHYQIVQDTYNSTDYFHIDSSSGLILTARMLDHEL 2356

Qy 309 GCWNEHTLERHIRTVAQSDETL--QMIASMKIKEAXPHVPIFDRYINREYILVLSNK- 365
Db 2357 ---VQHCTLK---VRSIDSGFPLSLSEVLVHIYISDVNDNPPVFNQLIYESYVSELAPRG 2410

Qy 366 -----MQKVVNDNPNFDVNFRIANVANVELILNTRCENPDNDRTPF 407
Db 2411 HFVTCVQASDADSSDFDRLEYSLISG-----NDRTSF 2442

RESULT 11
US-10-025-225-6
; Sequence 6, Application US/10025225
; Patent No. 6852844
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Miracar
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6852844el Human Protocadherin Proteins and Polynucleotides Er
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0285-USA
; CURRENT APPLICATION NUMBER: US/10/025,225

```

Db 2063 LRVARVVVRVNI--EDINDNSPVFVGLPYAAVQVDAEPCGLIVQVTAIDK-DKGPNGEV 2119
Qy 116 LWVL-----DSGLVNTQPMCS-----KLTFDLTTSQLLKQVEIPHDVA 156
Db 2120 TVVLQDDYGHFEINPNSGNVILKEAFNSDLNIEYGVITLAKDGGKPSLSTSVELPITIV 2179
Qy 157 VNATTGKRLSSLAVALDNCNTSDTM-VYIADEKGBGLVYVHNSDDSFHRLTSNTFYD 215
Db 2180 NKAMPVDPKPYFASVNEIDRMNIPILSINATSPGQGIIVIIDGDPFKQF---NIDFD 2236
Qy 216 PKFTKMT--IDGE-----SYTAQDGISS-----MALSPMTNN--LYYSPVASTSL 256
Db 2237 TGVLVKSPLDYEVTSAYKLIRASDALTCARAEVTVDLLVNDVNDNPPIDFQDPTVNTTL 2296
Qy 257 ---YVNTGEQRT---SDVQOND-IHYEGVQNLDTQSSAKVVKSGVLFPGLVGDAL 308
Db 2297 SEASLIGTPVLQVVISIDADSENKMWYQIVQDNTSDYFHDSSGSLILTARMLDHEL 2356
Qy 309 GCWNEHRTLERNHIRTVAQSDTL--QMIASMKIKEAXPHVIPDRYINREYILVLSNK- 365
Db 2357 ---VQCTLK---VRSDSGFPLSSEVLVHIYISDVNDNPPVFNQLIYESYSELAPRG 2410
Qy 366 -----MOKMVNDFNFDVFRIMNANVNELLILNTRCENPDNDRTPF 407
Db 2411 HFVTCVQASDADSDDFRLEYSILSG-----NDRTSF 2442

RESULT 13

US-10-025-225-2

; Sequence 2, Application US/10025225

; Patent No. 6852844

; GENERAL INFORMATION:

; APPLICANT: Yu, Xuanchuan

; APPLICANT: Miranda, Miracar

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6852844el Human Protocadherin Proteins and Polynucleotides En

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0285-USA

; CURRENT APPLICATION NUMBER: US/10/025,225

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: US 60/257,257

; PRIOR FILING DATE: 2000-12-20

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 4589

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-025-225-2

Query Match 4.7%; Score 103; DB 2; Length 4589;
Best Local Similarity 19.4%; Pred. No. 14;
Matches 79; Conservative 78; Mismatches 162; Indels 88; Gaps 19;

Qy 62 LRYNGVPSSLNVISKVGDGGLLPQYDWSFAKYDCCSGIVSASKLAIDKCDR----- 115
Db 2063 LRVARVVVRVNI--EDINDNSPVFVGLPYAAVQVDAEPCGLIVQVTAIDK-DKGPNGEV 2119
Qy 116 LWVL-----DSGLVNTQPMCS-----KLTFDLTTSQLLKQVEIPHDVA 156
Db 2120 TVVLQDDYGHFEINPNSGNVILKEAFNSDLNIEYGVITLAKDGGKPSLSTSVELPITIV 2179
Qy 157 VNATTGKRLSSLAVALDNCNTSDTM-VYIADEKGBGLVYVHNSDDSFHRLTSNTFYD 215
Db 2180 NKAMPVDPKPYFASVNEIDRMNIPILSINATSPGQGIIVIIDGDPFKQF---NIDFD 2236
Qy 216 PKFTKMT--IDGE-----SYTAQDGISS-----MALSPMTNN--LYYSPVASTSL 256
Db 2237 TGVLVKSPLDYEVTSAYKLIRASDALTCARAEVTVDLLVNDVNDNPPIDFQDPTVNTTL 2296
Qy 257 ---YVNTGEQRT---SDVQOND-IHYEGVQNLDTQSSAKVVKSGVLFPGLVGDAL 308
Db 2297 SEASLIGTPVLQVVISIDADSENKMWYQIVQDNTSDYFHDSSGSLILTARMLDHEL 2356

Qy 309 GCWNEHRTLERNHIRTVAQSDTL--QMIASMKIKEAXPHVIPDRYINREYILVLSNK- 365
Db 2357 ---VQCTLK---VRSDSGFPLSSEVLVHIYISDVNDNPPVFNQLIYESYSELAPRG 2410
Qy 366 -----MOKMVNDFNFDVFRIMNANVNELLILNTRCENPDNDRTPF 407
Db 2411 HFVTCVQASDADSDDFRLEYSILSG-----NDRTSF 2442

RESULT 14

US-09-134-001C-3150

; Sequence 3150, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3150

; LENGTH: 471

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3150

Query Match 4.7%; Score 102; DB 2; Length 471;
Best Local Similarity 20.8%; Pred. No. 0.4;
Matches 64; Conservative 38; Mismatches 112; Indels 94; Gaps 11;

Qy 99 CSGIVSASKLAIDKCDRLVLDLGLVNTQPMCSPKLLTF-----DLTTSQLLKQVEIPHD 154
Db 13 CDSMIKQKLYK-----WMLITLITFTILLFCLIIIFPKDTLASSEIDEAERSND 67
Qy 155 VAVNATTGKRLSSLAVALDNCNTSDTMVYIADEKGBGLVYVHNSDDSFHRLTSNTFYD 214
Db 68 IA-NLPHSKS-LSDISALDLNASLENFQELIYDCKGRKLIQTSN-----DNTLAY 116
Qy 215 DPKFTKMTIDGESYTAQDGISGMALSPMTNNLYYSPVASTSLYVNTGEQRTSDYQQNDI 274
Db 117 DNKIDFKHPRHIHQSHGIN-----YLVITEPIRSKDFSGYSV 155
Qy 275 HVEGVQNLDTQSSAKVVKSGVLFPGLVGDLSALGCWNEHRTLERNHIRTVAQSDTLQOM 334
Db 156 LVHSLQVYDNLVKSLEYVA---LAFGLIA-----TIITAGVS----- 189
Qy 335 IASMKIKEAXPHVIPDRYINREYILVLSNKQKQKQVNDNFDDVFNFRIMNANVNELLILN 394
Db 190 -----YIFSSQITKP-IVTMSNKQKQIRRDGQ-----NKLELT 222
Qy 395 TRCENPDN 402
Db 223 TNYEETDN 230

RESULT 15

US-09-134-000C-4939

; Sequence 4939, Application US/09134000C

; Patent No. 6617156

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 032796-032

; CURRENT APPLICATION NUMBER: US/09/134,000C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/055,778

```

; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4939
; LENGTH: 789
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-4939

Query Match      4.7%  Score 101.5;  DB 2;  Length 789;
Best Local Similarity 20.1%;  Pred. No. 1.1;
Matches 100;  Conservative 70;  Mismatches 138;  Indels 189;  Gaps 26;

QY 29 ERRQDAILSGEYDYKNYPSPDIDQMDHKIEFTMLRYNGVPSSLNVISKYVGGGPLLQPY 88
Db 264 KERRDVVLYTMYDNKKISAE---YEKAKATPIDEGLVPLKASDDNRKVVDD----- 311

QY 89 PDWSFAK-----YDCSGIVSASKLAIDKCDRLWLVDLSGLVNNTPQMCSP- 133
Db 312 ---NYVKEVINEVKAKTGKNVYTD--GLDIYTNLDMNAQKQLY-----DIVNSDQYVAFPD 362

QY 134 ----KLLTFDLTTSOLLKQV--ETPHDY-----AVNATTGKGRLLSSL-----AV 171
Db 363 DKMQVASTVIDVASGGVRAQIGGRHIPDDVOLGNLAVNTQRDVG--STVKPIMDYGPAI 420

QY 172 QSLDCNT-----NSD-----TWVYIADEKG-- 191
Db 421 ENLNYSTGRMLWVKPTKYPGTDIDVFNSDLTYQGVITMRRAIMGSRNTTAVQTFDEVGKE 480

QY 192 -----EGLIVYHNSDDSFRLTSNTFDYDPKFTKMTIDGESYTAQDGISGMALSP----- 241
Db 481 NIMPFITKGLGIDYKNLEASNAISSNTSD-----VDGDKY-----GISSLKLAAYAA 527

QY 242 -MTNNLYSPVASTSLYVNTQFR---TSDYQONDHYEGVQVQNILDQTS-----SAKVY 292
Db 528 FANNGIYNKP-----YYNKKVFNDSYDYQF-----DCKRAMKDSYAYMTMLKDV 576

QY 293 SKSGVLFFGLVGDPSALGCMNEHRTLERHNIPTVAQSDETLQMIASMKIKEAXP----- 345
Db 577 LGGTGFNGAIPG-----LIQAAKTGTSTNYTDEDLARMGTTE-KGIAPDSTFVG 625

QY 346 -----HVPIFDY-----INREYILVLSNKMCKMNNDFNFDVNFPRIM 384
Db 626 TTHYAVSVWMTGYNDRNTPYQYGYIASDYREIMSYLS---QNVSNDDWVQPSVVVRV- 681

QY 385 NANVNELILNRCENPD 401
Db 682 ---GNELYVKDAYEVPN 695

```

Search completed: May 3, 2006, 19:12:01
Job time : 46.6142 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:10:39 ; Search time 144.89 Seconds
(without alignments)
1190.997 Million cell updates/sec

Title: US-10-525-567-4
Perfect score: 2178
Sequence: 1 NILRGSLSKSLPILHEWKF.....NTRCENPDNDRTPFKISHL 413

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	452.5	20.8	541	6	US-11-097-143-7173
2	448	20.6	438	6	US-11-097-143-7005
3	435.5	20.0	453	6	US-11-097-143-40164
4	422	19.4	426	6	US-11-097-143-25233
5	415	19.1	412	6	US-11-097-143-20991
6	411.5	18.9	415	6	US-11-097-143-20973
7	366	16.8	429	6	US-11-097-143-28038
8	358	16.4	530	6	US-11-097-143-42198
9	357	16.4	379	6	US-11-097-143-41712
10	343.5	15.8	409	6	US-11-097-143-25236
11	331.5	15.2	316	6	US-11-097-143-1674
12	258	11.8	393	6	US-11-097-143-699
13	233	10.7	382	6	US-11-097-143-32673
14	229	10.5	394	4	US-10-481-180-17
15	209.5	9.6	400	4	US-10-481-180-18
16	177	8.1	388	4	US-10-156-761-7699
17	156	7.2	342	6	US-11-097-143-16716
18	122.5	5.6	575	4	US-10-724-972A-7483
19	116	5.3	946	4	US-10-032-585-7900
20	112.5	5.2	1252	4	US-10-354-774-52
21	112.5	5.2	1252	4	US-10-271-012-52
22	112.5	5.2	1252	4	US-10-452-024-128
23	112.5	5.2	1252	4	US-10-729-122-52
24	112.5	5.2	1252	4	US-10-729-039-52
25	112.5	5.2	1252	5	US-10-729-527-52
26	112.5	5.2	1252	5	US-10-727-898-52
27	112.5	5.2	1252	5	US-10-728-696-52

28	112.5	5.2	1252	6	US-11-001-241-52	Sequence 52, Appl
29	111	5.1	4643	6	US-11-097-143-41619	Sequence 41619, A
30	110.5	5.1	1250	4	US-10-354-774-50	Sequence 50, Appl
31	110.5	5.1	1250	4	US-10-271-012-50	Sequence 50, Appl
32	110.5	5.1	1250	4	US-10-729-122-50	Sequence 50, Appl
33	110.5	5.1	1250	4	US-10-729-039-50	Sequence 50, Appl
34	110.5	5.1	1250	5	US-10-729-527-50	Sequence 50, Appl
35	110.5	5.1	1250	5	US-10-727-898-50	Sequence 50, Appl
36	110.5	5.1	1250	5	US-10-728-696-50	Sequence 50, Appl
37	110.5	5.1	1250	6	US-11-001-241-50	Sequence 5, Appl
38	110.5	5.1	1251	4	US-10-452-024-5	Sequence 124, App
39	110.5	5.1	1251	4	US-10-452-024-124	Sequence 129, App
40	110.5	5.1	1251	4	US-10-452-024-129	Sequence 125, App
41	110.5	5.1	1252	4	US-10-452-024-125	Sequence 10, Appl
42	110.5	5.1	1252	4	US-10-205-516-10	Sequence 126, App
43	110.5	5.1	1255	4	US-10-452-024-126	Sequence 71379, A
44	110	5.1	391	4	US-10-282-122A-71379	Sequence 130, App
45	110	5.1	742	5	US-10-745-237-130	

ALIGNMENTS

RESULT 1
US-11-097-143-7173
; Sequence 7173, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7173
; LENGTH: 541
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-7173

Query Match 20.8%; Score 452.5; DB 6; Length 541;
Best Local Similarity 30.3%; Pred. No. 2.5e-31;
Matches 125; Conservative 90; Mismatches 150; Indels 47; Gaps 17;
Qy 16 HEWKFFDYFGSDRRQDAILSGEYDYKNYPSIDQWHDKIFVTMLRY-NGVPSSLNVI 74
Db 29 YSWSQLDFAFENTRLKQALASGDYIFQNALPVGHEHFNRLFTVTPKWRDGPATLTYI 88
Qy 75 S-KKVGGGPLQYPPDWSFAKYDDC-SGIVSASKLAIDKCDRLWLDLSGLV---NNTQP 129
Db 89 NMDRSLTGSPELIYPDWRNSNTAGDCANSITTAIRIKVDEGRLWLDLTGTGIGNTTIN 148
Qy 130 MCSPKLLTFDLTTSQLLKQVEIPHDVAVNATTGKRLSSLAQSLDCNTN-SDTWVYIAD 188

Db 149 PCYAVNVFLDTTDIRRYELP-GVDTNPNT---FTIANIIV---DIGKNCDDAYAFAD 201
QY 189 EKEGGLIVYHNSDDSPHRLTSNTFDY-DPKFTKMTIDGESYT-AQDGISGMALSPMTNN- 245
Db 202 ELGYGLIAYSWELNKSXWFAHSAHYFFPDPLRGDFNVAGINFQWGEIGFMSLPSIRSDG 261
QY 246 ---LYYSPVASTSLYYVNT---EQFRTSYQONDHYEGVQNILDTQSSAKVYKSGVL 298
Db 262 YRTLYFSLASHRQFAVSTRILRDETRTDSYHDFVALD--ERGPSHTTSRVMSDDGIE 319
QY 299 FFLGVGDSALGCWNEHRTL---ERNIRTVQASDETLQMIASMKIEXAPHVPIFDRIY 354
Db 320 LFNLDIQNAVGCW--HSSMYPSPQFHGI--VDRDDVGLVFPADVKIDB----- 363
QY 355 NREYILVLSNMQKMNNDNFDDVFNPRIMNANVNELINLNRCPNDNDRT 406
Db 364 -KNVWVLSDRMPVFLSLDLDYSDTNFRIYTAFLATLIENTVCDLRNNAVGP 414

RESULT 2

US-11-097-143-7005
; Sequence 7005, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7005
; LENGTH: 438
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-7005

Query Match 20.6%; Score 448; DB 6; Length 438;
Best Local Similarity 28.8%; Pred. No. 4.6e-31;
Matches 123; Conservative 67; Mismatches 169; Indels 68; Gaps 10;
QY 18 WKFDYDFGSDERRQDAILSGEYDYKKNYPSDIDQWHDKIFVTMLRYN-GVPSLSNVISK 76
Db 33 WKQAFDWPTEAEAEAKSGHYIVENNLPLGVERWQNRIFVTVPWKAGVAATLNYIDI 92
QY 77 KVGGGPGLQPDWSPAK-----YDCSGIYSASK 107
Db 93 NSTEKSPKLPHPYSWEANKLPIDVQPDQKTPSGRLDADKAQDAGIQLKDNSTWISTFR 152
QY 108 LAIDKCDRLWLDSPQMCSPK-----LLTFDLTTSQLLKQVEIPHVDVAVNATT 161
Db 153 IQVDVCDRLWLDLGLAD---ILGSPKQITPNSILVFDLTKDTLLRFTTIPAD-----QT 204

QY 162 GKRLSSLAQSLDCNTNSDTPWYIADKEGGLIVYHNSDDSPHRLTSNTFDYDPKFTKM 221
Db 205 KEDSFFANIVVDADRSECQDAFYIIDLGAIVGIVYSLRNDKSYRVKHNFFHFDPLHGD 264
QY 222 TIDGESYTAQDGISGMALSPM---TNNLYYSPVASTSLYYVN-----TEQFRTSYQON 272
Db 265 NVGCVNFQWTDGVFLGAVGEMDPDKDIYFHALASTKFKVSNRVLQNEHSHVTAGDSYY 324
QY 273 DIHYEGVQNILDTQSSAKVYS-KSGVLFFGLVGDLSALGCWNEHRTLERNHIRTVAOSDET 331
Db 325 DKYVVGDRG-MNQSTAEVFDPEGTGIVFTVQVKNDAICWNIKRPTPTDQGLIDSDSHT 383
QY 332 LQMIASMKIEXAPHVPIFDRIYINREYILVLSNMQKMNNDNFDDVFNPRIMNANVNEL 391
Db 384 LVFPNDMKID-----NEGTVIWLSDKMTPLYKELDPDSAVNRYILMQNRDL 430
QY 392 ILNTRCE 398
Db 431 IKGTPCE 437

RESULT 3

US-11-097-143-40164
; Sequence 40164, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40164
; LENGTH: 453
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-40164

Query Match 20.0%; Score 435.5; DB 6; Length 453;
Best Local Similarity 28.4%; Pred. No. 6.3e-30;
Matches 116; Conservative 85; Mismatches 165; Indels 43; Gaps 12;
QY 9 NKSLPILHEWKFPDYDFGSDERRQDAILSGEYDYKKNYPSDIDQWHDKIFVTMLRY-NGV 67
Db 19 NDNLVAYEWREMDFKYANPDQRWSAIERGEFKPANVIPPFGLEVAGHRLFTVLPWRMDGV 78
QY 68 PSS-----LNVISKYVGDGGLPQPYDMSFAKYDDCS-GIVSASKLAIDCDRLWLD- 120
Db 79 PASLAYLDLNDTSSK---GPAKLPFSPQWQAHNLQEAPELVPFVRADRCRGLWIDS 134
QY 121 --SGLVNNTPQMCSPKILTFDLTTSQLLKQVEIPHVDVAVNATTGKGRSLSLAVQSLDCNT 178
Db 135 RISGVLEQTKIYGAQLVYVLDLHNDLLRR-----HVLPAQLKQGSLLANLAVEDSDC-- 188

```
QY 179 NSDTMYIADKEGGLIVHNSDDSPHRLTSNTFDYDPKFTKMTIDGESYTAODGISGWA 238
Db 189 -ENTFAYADLGSPLGLVYVSWKDEESWRVQHHPFHPDPMAGNFSINGIEFQWDDGLYGLA 247
QY 239 LS-PMTN---NLVYSPVASTSLVYVNTQFRTSDYQONDIIHYEGVQNI-----LDTQSSAK 290
Db 248 LSKPLETGATLVPFLCSTTESVDTSLRNKTLATSPMIYEFKVLGSRGENTQAGAE 307
QY 291 VVS-KSGVLFFGLVGDGALGCVNNEHRTLERHNIRTVQAQSDTETQMIAKXPHVPI 349
Db 308 FLDPDGTGLFYPALPNLNEVACWRTATDFSHSSQSRIHMNDTLVFPSPDIKVD-----360
QY 350 FDIYINREYILVLSNKMOKMVNDFNFDVDFRIMANVNELILNTRCE 398
Db 361 -----QKRLWVLSNQLPVFIYDELVYAGSINFRILTASVKEAIENTACE 403

RESULT 4
US-11-097-143-25233
; Sequence 25233, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25233
; LENGTH: 426
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-25233

Query Match 19.4%; Score 422; DB 6; Length 426;
Best Local Similarity 26.8%; Pred. No. 9.3e-29;
Matches 112; Conservative 83; Mismatches 171; Indels 52; Gaps 13;

QY 10 KSLPILHEWKEFPDYDFGSDERQDAILSGEYDYKNVPSDIDQWH-----DKIFVTMLR 63
Db 30 RDTPIVFEWKNLQGFPEQSDQVLRNGRYNPDSPIPIDIVYPPNPGGPPHFVTSR 89
QY 64 Y-NGVPSLNVISKVGDGGLLPYP--DWSFAKYDDCSGIVSASKLAIDKCDRLWYLD 120
Db 90 FQGGVPSLGVYVNVQRENGEIQAYPSYQWSSHGANGCDGLTSYVRVHIDACGQWYLD 149
QY 121 SGLVNNTPQMSCPKLLTLDLTSQLLKQVEIPHDVAVNATTGKRLSSLAQSLDCTN- 179
Db 150 SGEIEFVQ-HCAQVQWVFLATDQLIHYRLPE-----TSYKAVSRFVNIFADIRDP 202
QY 180 -----SDTMVYIADKEGGLIVHNSDDSPHRLTSNTFDY-DPKFTKMTIDGESYTAODG 233

QY 203 PSQCCKDFAYLADPTSKAIVVYDVVGQSSWRI-ENKFTYVDAKFGTHTVAGSFELLGD 261
QY 234 ISGMALSP---MTNNLYYSPVASTSLVYVNTQFRTSDYQONDIIHYE-GVQVILD---- 284
Db 262 PLAMATTPGLGLGRRLHIFHALSN-----ELELAIPDLILNATNWKQGLSSLSSEFTV 315
QY 285 -----TQSSAKVVSXSGVLFFGLVGDGALGCVNNEHRTLERHNIRTVQAQSDTETQMIAK 339
Db 316 LGRKGIQASHAISRQGLFCGFLPIGFIQWDIRRPYNRENKVLAINPATLQFVSGMK 375
QY 340 IKAEXPHVPIFDRIYINREYILVLSNKMOKMVNDFNFDVDFRIMANVNELILNTRC 397
Db 376 IVERPAD-----GREELWLLSDRLQKIFAGTIDYREINRYVMRCDVDDLLQGRCC 425

RESULT 5
US-11-097-143-20991
; Sequence 20991, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20991
; LENGTH: 412
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-20991

Query Match 19.1%; Score 415; DB 6; Length 412;
Best Local Similarity 29.7%; Pred. No. 3.7e-28;
Matches 120; Conservative 71; Mismatches 161; Indels 52; Gaps 14;

QY 22 DYDFGSDERQDAILSGEYDYKNVPSDIDQWH-----DKIFVTMLRY-NGVPSLNV 74
Db 32 ELEFPSPQERQALRDGLDYGSPVIDVDVYKHGDATPSIFVTIPFAKGVPSLAYV 91
QY 75 SKYVGDGGLLPYP--DWSFAKYDDCSGIVSASKLAIDKCDRLWVLDGLVNNTPMCS 132
Db 92 TNEMRPNGTLLOAYPSYVSWKDEESWRVQHHPFHPDPMAGNFSINGIEFQWDDGLYGLA 150
QY 133 PKLTLDLTSQLLKQVEIPHDVAVNATTGKRLSSLAQSLDCTNSDTMYIADKE 192
Db 151 POLVAIDLESKVAHQVQKPKRL---YKEGVSRFVTPTVE-LDPHNCVDFVYMAISIGD 206
QY 193 GLIYVHNSDDSPHRLTSNTFDY-DPKFTKMTIDGESYTAQDGISGMALSPM-----TNLY 247
Db 207 GIVYDVAAQSSWRI-ENKFTYVDAKFGTHTVAGSFELLGD 265
QY 248 YSPVAS-----TSLVYVNTQFRTSDYQONDIIHYEGVQVILD-----TQSSAKVVS 293
```

Db 266 FHSLSSEWQMAIPLDVVN-----NGSNWRLND-----VSAALDQFOLLKGGKSGQCVAAMS 316
QY 294 KSGVLFFGLGDSALGCWNEHRTLERINIRTVAQSDTLQMIASMKIKEAXPHVIPIDRY 353
Db 317 ESGFLICGLQPSALLAWNIRTVGSHQNLVWLVEDEQRLQFASGLKIVR-----NH 367
QY 354 INREYILVLSNKQKQVNNDFNFDVNNFRIMNANVNELILNTRC 397
Db 368 EGKEELWVLSNRLQKAFGAGLDYKEINFRIQKCGVQELLSGRPC 411

RESULT 6

US-11-097-143-20973
; Sequence 20973, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20973
; LENGTH: 415
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-20973

Query Match 18.9%; Score 411.5; DB 6; Length 415;
Best Local Similarity 28.0%; Pred. No. 7.7e-28;
Matches 119; Conservative 74; Mismatches 147; Indels 85; Gaps 15;
QY 5 GESLNSKLPI-----LHEWFFDYDFGSDRRQDAIISGEYDKNNYVPSIDQWH----- 54
Db 19 GVGNGRPRVRYVETLTQWGLEFGFPTAQDRENAQAAGNLVPENGTFIDVQPYMWANGQ 78
QY 55 DKIFVTMLRY-NGVPSLSNIVSKVGDGGLLPQYPD--WSFAKYDDCSGIVSASKLAID 111
Db 79 IRLFTTIPRVTGIPYTLATVSATQNGEFLQPYPNYSWHNANGEDCCDITSAFRAVIT 138
QY 112 KCDRLWLVDGLVNNTQPMCSKLLTFDLTTSOLLKQVEIPHVDVANNATTGKRL-----S 167
Db 139 ECNQMWVIDSGVIGTTQ-LCPQOLLQPALATDRLHFRFPNDTYIPS-----GSLFITPN 193
QY 168 SLAVQSLDCNTSDTMVYIADEKGEGLIVYHNSDDSFHRLTSNTFDY-DPKFTKWTIDGE 226
Db 194 VLVDPPPRGTCRMTIYVADTSMR-----AENRFMPDPDYGKHTIAGE 238
QY 227 SYTAQDQISGWSALSPMTNNIYSPVASTLSYYVN-----TQFRTSDY 269
Db 239 SFYLMQGM--FALNNDKRNLYFHPLASASEYSVPLSALNRQQNWANGPEALPEEFRLGR 296

QY 270 QQNDIHVEGVQNTLDQTSSAKVYKSGVLFFGLVGDALGCWNEHRTLERINIRTVAQSD 329
Db 297 RRS-----ECAASAIIDGRNNVYCVTFNPVKLF-----VWNVSPYNSRNFGLNPAKS 343
QY 330 ETQLQMIASMKIKEAXPHVIPIDRYINR---EYILVLSNKQKQVNNDFNFDVNNFRIMNA 386
Db 344 DDLQFVSGMKVLR-----NREGQEELWMLSNRYOKIAAGTILNSKEVNFRLRR 391
QY 387 NVNEL 391
Db 392 KLDDV 396

RESULT 7

US-11-097-143-28038
; Sequence 28038, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28038
; LENGTH: 429
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-28038

Query Match 16.8%; Score 366; DB 6; Length 429;
Best Local Similarity 27.6%; Pred. No. 9.5e-24;
Matches 105; Conservative 68; Mismatches 169; Indels 38; Gaps 12;
QY 37 SGEDYDKNNYVPSIDQWHDKIFVTM-LRYNGVPSLSNVI--SKKVGDDGGLLPQYDMSF 93
Db 70 SSGFIQVNNYVPSIDQWHDKIFVTM-LRYNGVPSLSNVI--SKKVGDDGGLLPQYDMSF 129
QY 94 AKYDDC-SGIVSASKLAIDKCDRLWLVDGLV---NNTQPMCSKLLTFDLTTSQLLKQV 149
Db 130 NQVNASQNLVSIVYRVSVDVCGRLMFDVTGMLBFFPNRQIRHPSIWIVIDLANDRLKRF 189
QY 150 EIPHDVAVNATTGKRLS-SLAVQSLDCNTNSDTMTVYIADEKGEGLIVYHNSDDSFHRLT 208
Db 190 EIFQSI---VEIGRGLASITIDVGARRCN---DAYAYIPDLVNRRLHVYHLRSDRIWSFE 243
QY 209 SNTFDYDPKFTKMTIDGESYTAODGIGSMALSPM---TNNLYSPVASTLSYYVN--- 261
Db 244 HSFNFDPDLNLDNINIGQTFRWDGDFSATLSGYKPDGSDRVDFFHFMASNEFVVSNRVL 303
QY 262 -EGRFT--SDYQQNDIHVEGVQNTLDQTSSAKVYKSGVLFFGLVGDALGCWNEHRTLE 318
Db 304 QQEFNAARSDH-GDDFHLLGTRGPTQSTQSTMHKYDPRITGVIFFAEVQKSGVGCWKTSKPF 362


```
Qy 319 RHNIQTVAQDETLQMIASMKIEXAPHVIFDRIYNREYILVLSNKKQKVNNDNFDD 378
Db 363 TENHGSYNSSEMIYPSDLTIDE-----EGYIWNWSNMPFVYSKLDVEK 409
Qy 379 VNFRIIMANVNELILNTRCE 398
Db 410 YNFRIMQSTILLAKRGTVCE 429

RESULT 8
US-11-097-143-42198
; Sequence 42198, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-03-23
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42198
; LENGTH: 530
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-42198

Query Match 16.4%; Score 358; DB 6; Length 530;
Best Local Similarity 23.0%; Pred. No. 6.8e-23;
Matches 107; Conservative 91; Mismatches 170; Indels 98; Gaps 16;

Qy 6 ESLNKSPLIHEWFFDYDFGSDERRDQAILSGEYDYKYNYPSPSIDQWHDKIFV-TMLRY 64
Db 19 QALTPLQLQVAKQKLLRYNFEPAQVSD---PNFYNPQNLITGLAVDDRIFVATPKLF 75
Qy 65 NGVPSLNVISKVGGDGPGLQYPDPWFAKYD-----DCSGIV--SASKLAIDKCDRLAV 118
Db 76 SGVPSTSVSWKAQFGDSFTLNAFPDWTFSNTGRSDFNCSDLILTSVYRLRVDSNRIWL 135
Qy 119 LDSGL---VNNTPMCSPKLLTFDLTTSQLLKQVEIPHVDV-----AVNATTGKGR 165
Db 136 LDAGISRLSEDEYITCPKILVVDLATRVVRIDFPPEVLREGESLFTNNWIDETAKG- 194
Qy 166 LSSLAVQSLDCNNTSDTMVYIADEKGEGLIVYHNSDDSFHRLTSTNTFDYDPKFTQMTIDG 225
Db 195 -----CD---DVFYITDTEPGIIVYDSCGVTKWRVSHAMPYDPDPFAQSEIHE 241
Qy 226 ESYTAQDGLSGMALSPMTNNLYSPVASTLSLYVNTQEPTS---DYQNDIHYEGVQNI 282
Db 242 HRFVLMDGVGLTFDERTGVVYFQPLATDRVFSVHKVNLRAGLPDGKMLDVKLVGKKS- 300
Qy 283 LDTQSSAKVSK-SGVLFFGLVGDALGQWNEHRLTLERHNIQTVAQDETLQMIASMKIK 341
```

```
Db 301 --SQGIGLAVSPDSSLIFSPLETAIASWNP--TTNQSV--LAPDRDQLQFVADITTT 354
Qy 342 EAXPHVPIPDRIYNREYILVLSNKKQKVNNDNFDDVFRIM----- 384
Db 355 KSEPGV-----IYAIASKFHRFFLKNLNPNEFNRIYVRLLELPAGNSLGLHGRVAL 403
Qy 385 -----NANVNELILNTRCE-----NPDNDRTPFK 408
Db 404 PAPPTHNSLLNYGVFNTHGQASTNALQTYFTSPALTTPTFTTKSPFK 449

RESULT 9
US-11-097-143-41712
; Sequence 41712, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-03-23
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41712
; LENGTH: 379
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-41712

Query Match 16.4%; Score 357; DB 6; Length 379;
Best Local Similarity 27.3%; Pred. No. 5.1e-23;
Matches 102; Conservative 71; Mismatches 162; Indels 38; Gaps 13;

Qy 44 NNYPSDDIDQWHDKIFVITMLRYN-GVPSLNV--SKKVGDDGGLLQYPDWSFAKYD-DC 99
Db 27 NNVPWGATHFGRGLFVTPRRRGVGPSTLNTIDLAEDGSGNSRSPKURAYPNPALNDFNABA 86
Qy 100 SGIYSASKLAIDKCDRLAVLSDGLV---NNTQPMCSPKLLTFDLTTSQLLKQVEIPHVA 156
Db 87 ENLVSVYTSVDACORLWFIDTGMLEYFNRRQIRPSIWWVDLATDQVLKFDVPESI- 145
Qy 157 VNATTGKRLSSLAVQSLDCNNTSDTMVYIADEKGEGLIVYHNSDDSFHRLTSTNTFDYDP 216
Db 146 --AETGRG-LASITV-DVKAGCQGDAYAVIPDLVYRRLVYVHLRNDWSFEHNYFNFD 201
Qy 217 KFTMTIDGESYTAQDGLSGMALSPM---TNNLYSPVASTLSLYVNTQEPR-----T 266
Db 202 LSGDLISIGQGFRRWDGIGFISITLGAQKLDGSDAYFHPMASTNEFVSVNRVQQSSNAAR 261
Qy 267 SDYQNDIHYEGVQNIQTQSSAKVSK-SGVLFFGLVGDALGQWNEHRLTLERHNIQT 325
Db 262 SDH-CHNDFRVLGSRG-PTQSTMHAYDPGTGVIFDEIQRGVGCWTKSKPISAENYGSV 319
Qy 326 AQSDETLQMIASMKIEXAPHVIFDRIYNREYILVLSNKKQKVNNDNFDDVFRIM 385
```



```

; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32673
; LENGTH: 382
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32673

Query Match      10.7%; Score 233; DB 6; Length 382;
Best Local Similarity 24.3%; Pred. No. 6.3e-12;
Matches      83; Conservative      62; Mismatches 143; Indels      54; Gaps      12;

Qy      11  SLPLHEWKFDFDGSERRQDAILSGEYDYKNNYPSDIDQWHDKIFVTWMLRY-NGVPS 69
Db      36  SQPI--QMTGGQFEPCASTSLFKSGKFPKVIATRAQLIGDTIYALPRYKGVPA 93

Qy      70  SLNVISKVGGGGLLOPYDPWSPAKYDDCSGIVSASKLAIDKCDRLWLDGLVNTQP 129
Db      94  TLVKTSTKPGCTCTTFKPYPCWDLQEEGNCALQSVVDLVVDQNEVLWLDGIVNTLET 153

Qy      130  ---MCSPKLLTFDLTTSOLLKQVEIPHDAVNATGKGRSLSSLAQSLDCNTNSDTMYI 186
Db      154  PVRKCPKPVAMSVKTKGLKTVSL-----GLTSSNSRLQYLV--DYAPDGGCFYV 205

Qy      187  ADEKGEGLIVYHNSDDSFHR-----LTSNTFDYDPKFTKMTIDGESYTAQDGISGMALS 240
Db      206  SDAANRAIIVYNLQADRGFRVVLPAVTKAGCRSDVLY-----IALIRRD 250

Qy      241  PMTNLYSPVASTSLYVNTTEQRTSDYQNDIHYEGVQN--ILD--TQSSAKV---S 293
Db      251  CGSTELYFTVLTSLNKLFSLKSEYLR-----GVADGRILDGKPSRMVIGTD 299

Qy      294  KSGVLFGLGDSALGCWNEHRTLERNIRTVACSDTELQMI 335
Db      300  NGSIAIFRNEGDAEYVRWDTNSTFVEANFKPVYRS-QTCQLV 340

RESULT 14
US-10-481-180-17
; Sequence 17, Application US/10481180
; Publication No. US20040171821A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Belkaid, Yasmine
; APPLICANT: Kambawi, Shaden
; APPLICANT: Sacks, David

```

```

; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 699
; LENGTH: 393
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-699

Query Match      11.8%; Score 258; DB 6; Length 393;
Best Local Similarity 25.2%; Pred. No. 3.8e-14;
Matches      79; Conservative      58; Mismatches 124; Indels      52; Gaps      12;

Qy      35  ILSEYDYKNNYPSDIDQWHDKIFVTWMLRY-NGVPSLNVISKVGGGGLLOPYDPWSP 93
Db      68  VQSGRYVPRNVIVTRAQLQRDSAFVALPRYKQGVFTLGLKYNLKKGCCLTKIAPYPCWAI 127

Qy      94  AKYDDCSGIVSASKLAIDKCDRLWLDGLVNN--TOPM--CSPKLLTFDLTTSOLLKQVE 150
Db      128  QEEGNCQALQSVVDIAVDQNGLLWALDVGIVNTLEQPIRRCSPKIVAINTANHKVKSID 187

Qy      151  IPHDVAVNATGKGRSLSSLAQSLDCNTNSDTMYIADKGEGLIVYHNSDDSFHRLTSN 210
Db      188  LS-----DLVTSESLQFIVV---DYKDKNPFVYVADAGARSILVYDITGNKSYRVL- 238

Qy      211  TFDYDPKFTKMTIDGESYTA---ODGISGMALSPMTNLYSPVASTSLYVNTTEQRT 266
Db      239  ----PKATAPTSD-VLYVALTSKPDG-----TSTLFFSYLSSPRLYSIRGEYLRV 283

Qy      267  SDYQNDIHYEGVQNILDTQSAKVVSQGV-----LPFGVLGDSALGCWNEHRTL 317
Db      284  G-----QAGSIIDV--GPKPYGKQAVLLGADGTSLFFRYKGENDIYLWDSCTCF 332

Qy      318  ERHNIRTVACSD 330
Db      333  KAANLQEVQRGD 345

RESULT 13
US-11-097-143-32673
; Sequence 32673, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:

```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2006, 19:12:24 ; Search time 23.7942 Seconds
(without alignments)
803.371 Million cell updates/sec

Title: US-10-525-567-4

Perfect score: 2178

Sequence: 1 NILRGSLNKLPLHEWKF.....NTRCENPDNRTFPKISLH 413

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep.1*
- 2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep.*
- 3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep.*
- 4: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep.*
- 5: /SIDSS/ptodata/1/pubpaa/PCT NEW PUB.pep.*
- 6: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep.*
- 7: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep.1*
- 8: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.*
- 9: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep.1*
- 10: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep.*
- 11: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep.1*
- 12: /SIDSS/ptodata/1/pubpaa/US60 NEW PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276.5	12.7	397	9	US-10-533-811-29
2	260	11.9	388	9	US-10-527-500-51
3	256	11.8	388	9	US-10-527-500-5
4	240.5	11.0	393	9	US-10-527-500-7
5	240.5	11.0	412	9	US-10-533-811-23
6	214	9.8	393	9	US-10-527-500-49
7	184	8.4	399	9	US-10-533-811-63
8	113.5	5.2	1530	11	US-11-045-004-34
9	108.5	5.0	829	9	US-10-909-769-26
10	100.5	4.6	2314	11	US-11-097-728-2
11	100.5	4.6	2353	11	US-11-097-728-6
12	99.5	4.6	2376	11	US-11-096-051-4
13	99.5	4.6	2715	11	US-11-096-051-2
14	97.5	4.5	371	9	US-10-194-487-146
15	97.5	4.5	371	9	US-10-195-883-146
16	97.5	4.5	371	9	US-10-195-888-146
17	97.5	4.5	371	9	US-10-195-889-146
18	97.5	4.5	371	9	US-10-218-784-144
19	97.5	4.5	371	9	US-10-219-061-144
20	97.5	4.5	371	9	US-10-219-062-144
21	97.5	4.5	371	9	US-10-219-064-144

ALIGNMENTS

RESULT 1

US-10-533-811-29
; Sequence 29, Application US/10533811
; Publication No. US20060051364A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; APPLICANT: Barral, Aldina
; APPLICANT: Netto, Manoel
; APPLICANT: Brodskyn, Claudia
; APPLICANT: Gomes, Regis
; TITLE OF INVENTION: LU. LONGIPALPIS POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 4239-67028-08
; CURRENT APPLICATION NUMBER: US/10/533.811
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/422,303
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/US2003/034453
; PRIOR FILING DATE: 2003-10-29
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 29
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Lutzomyia longipalpis
US-10-533-811-29

Query Match 12.7%; Score 276.5; DB 9; Length 397;

Best Local Similarity 24.9%; Pred. No. 1.2e-15;

Matches 107; Conservative 68; Mismatches 165; Indels 89; Gaps 20;

QY	20	FFDYDFGSDER-----RQDAILSGEYDYKKNYPSD-----IDQWHDKIFVTM 61
Db	5	FFLYTFGLVQTFIGVEIKQGFKNKILY-EGDTSENFNPNNILTAFYADESQLFLTV 63
QY	62	LYRNGVPSLNVISK-----KVGDDGPLLQPYPDMSFAKYDDCSGIVSASKLAIDKC 113
Db	64	PR--KYPTMTLAEVDETEKNSFSGDTSPLL-----CKFSGHETGKELTSYQYVIDEC 116
QY	114	DRLWLDLSGLVNNT-----QPMCSPKLLTFLDTLTSQLLKQVEIPH-----DVAVNAT 160

Db 117 HRLWVVDVGSVERNSDGTGEGEPHNPTLVAVD-----LKEANYPEVIRVTFPDNSIEKP 170
Qy 161 TKGRLSSLAQSLLDCNTNSDTWYVIADEKGEGLIVY-HNSDDSFHRLTNTFDYDPKFT 219
Db 171 TFLGGFADVVKPDEC---SETFVYIINFLNALIVVDHKNKDSW-TVQDSTFGPKK-S 225
Qy 220 KWTIDGSEYTAQDQIGSMALSPWN-----NLYGSPVASTSLYYVNTQFRTSDYQNDIIH 275
Db 226 KFDHGGQYQYEAGIFGTLGERDNEGNRQAYYLVASSTKLHSINTKELQKGSKNV-AN 284
Qy 276 YEGVQNLDTQSSAKVVS-----KSGVLFGLVGDSALGCWNEHRTLRHNIRTVAAQSD 330
Db 285 YLG-----DRGESTAIGLVYDPKTKTIFVFNESKRVSCWNTQETLKNKIDVIYENAD 339
Qy 331 TLQMIASMKIEXPHVPIFDYRINREYILVLSNMOKMVAND-FNFDVDFNFRIMNANVN 389
Db 340 -FSFGTIDISID-----SQDNLWFLANGLPLENSDKFVTKPRYQIFKVNQI 385
Qy 390 ELILNTRCE 398
Db 386 EAIAGTKCE 394

RESULT 2

US-10-527-500-51
; Sequence 51, Application US/10527500
; Publication No. US20060004186A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; APPLICANT: Kamhawi, Shaden
; APPLICANT: Belkaid, Yasmine
; APPLICANT: Fischer, Laurent Bernard
; APPLICANT: Audonnet, Jean-Cristophe
; APPLICANT: Milward, Francis William
; TITLE OF INVENTION: P. ARIASI POLYPEPTIDES AND P. PERNICIOSUS POLYPEPTIDES AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 4239-66903-02
; CURRENT APPLICATION NUMBER: US/10/527,500
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/US2003/029833
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 60/425,852
; PRIOR FILING DATE: 2002-11-12
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Phlebotomus perniciosus
US-10-527-500-51

Query Match 11.9%; Score 260; DB 9; Length 388;
Best Local Similarity 23.5%; Pred. No. 2.9e-14;
Matches 96; Conservative 67; Mismatches 172; Indels 74; Gaps 14;
Qy 16 HEWKFFDYFGSDERRQDAILSGEYDYKNN-----YPSDIDQWHDKIFVTMLRYNGVPSL 71
Db 25 YAWKNISF-----EGIDPASYSVKNSIVTGFADADS--KKIFITIPRLNPVITL 73
Qy 72 NVI-SKKVGDGGLLPQYPDWSPFAKYDDCSGIVSASKLAIDKCDRLWVLSGLV-----N 125
Db 74 TELDTTHKPEGSPLSKFP-----GSKLISVYQVVIDECRLWIVDAGVYKGD 125
Qy 126 NTQWCSFKLLTFLTLTSQL--LKQVEIPHVDVAVNATTKGRLSSLAQVSLDCNTNSDTM 183
Db 126 QKIPKKNAAIAYDLTKDNYPEIDRYELPNNVAGNPLGFGGFAVDVTPNKEGC---GKTF 182

Qy 184 VYIADKSGEGLIVHNSDDSFHRLTNTFDYDPKFTMTIDGESYTAQDQIGSMALSPM- 242
Db 183 VYITNFEDNTLIVYDQEKDSWKISHDSFKPEHE-SILTHNGAQHILKLGIFGITLGDLD 241
Qy 243 ---TNLNYSPVASTSLYYVNTQFRTSDYQ-----QNDIHVEGVQNLDTQSSAKV 292
Db 242 EGNRQAYYLGGSSTKLFRVNTKDLKKAGQIBFTPLGRGSHSEALALAYD----- 293
Qy 293 SKSGVLFFGLVGDGSAALGCWNEHRTLRHNIRTVAAQSDETLQMIASMKIEXPHVPIFDR 352
Db 294 PKTKVIFFEYNSKRISQNTQKSLNPDNDIVYHSPDF-----IFGT 336
Qy 353 YINRE---YILVLSNKQKMNNDNFDDVNFPRIMNANVNLNTRCE 398
Db 337 DISMDSKLPWFPSNGHPPIENVLQTFDPKPHFLRLISMDTKKSIHGKCE 385
RESULT 3
US-10-527-500-5
; Sequence 5, Application US/10527500
; Publication No. US20060004186A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; APPLICANT: Kamhawi, Shaden
; APPLICANT: Belkaid, Yasmine
; APPLICANT: Fischer, Laurent Bernard
; APPLICANT: Audonnet, Jean-Cristophe
; APPLICANT: Milward, Francis William
; TITLE OF INVENTION: P. ARIASI POLYPEPTIDES AND P. PERNICIOSUS POLYPEPTIDES AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 4239-66903-02
; CURRENT APPLICATION NUMBER: US/10/527,500
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/US2003/029833
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 60/425,852
; PRIOR FILING DATE: 2002-11-12
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Phlebotomus ariasi
US-10-527-500-5

Query Match 11.8%; Score 256; DB 9; Length 388;
Best Local Similarity 24.0%; Pred. No. 6.3e-14;
Matches 98; Conservative 63; Mismatches 175; Indels 72; Gaps 15;
Qy 16 HEWKFFDYFGSDERRQDAILSGEYDYKNNYPSDI--DQWHDKIFVTMLRYNGVPSLNV 73
Db 25 YAWKNIYE-GIDQ-----GSYNIENSIPTAFADAAASKKIFITIPRINQVPTL 75
Qy 74 I-SKKVGDGGLLPQYPDWSPFAKYDDCSGIVSASKLAIDKCDRLWVLSGLV-----NNT 127
Db 76 FDSIKYPGSGPLSKFP-----GSDNIIISVYQVVIDECRLWIVDAGVYKGDQK 127
Qy 128 QPMCSFKLLTFLTLTSQL--LKQVEIPHVDVAVNATTKGRLSSLAQVSLDCNTNSDTM 185
Db 128 YPKKNPAIAYDLTKDNYPEIDRYELPINIAGNPLGFGGFTVDVTPNKEGC---GKTF 184
Qy 186 IADEKGEGLIVHNSDDSFHRLTNTFDYDPKFTKMTI--DGESYTAQDQIGSMAL-----S 240
Db 185 ITNFEDNTLIVYDQEKDSWKISHGSGF--KPEHESILIHNGVDHILKLGIFGITLGRDS 242
Qy 241 PMTNLNYSPVASTSLYYVNTQFRTSDYQNDI-----HYEGVQNLDTQSSAKVVS 293

Db 243 EGNRPAYLGGSSTKLFEVNTKALKKXGEIEPITLGDGRPHSEAIALAYD-----P 294

Qy 294 KSGVLPGLVGDSDALGWCNEHRTLERHNRITVAQSDTLQMIASMKIEXAPHVIPFDY 353

Db 295 KTKVIFTEYNSKISKISCNWTKKPLIHDNMOKIYASPEF-----IFGTD 337

Qy 354 I---NREYILVLSNMQMNVNDFDVFNFRIMANVNELLNTRCE 398

Db 338 ISVDSSEKLMFFSNGHPPIENLQSSDKPHLHLSVDETKAIRGCKCE 385

RESULT 4

US-10-527-500-7

Sequence 7, Application US/10527500

Publication No. US20060004186A1

GENERAL INFORMATION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS

APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND

APPLICANT: HUMAN SERVICES

APPLICANT: Valenzuela, Jesus G.

APPLICANT: Kanhawi, Shaden

APPLICANT: Belkaid, Yasmine

APPLICANT: Fischer, Laurent Bernard

APPLICANT: Audonnet, Jean-Cristophe

APPLICANT: Milward, Francis William

TITLE OF INVENTION: P. ARIASI POLYPEPTIDES AND P. PERNICIOSUS POLYPEPTIDES AND

TITLE OF INVENTION: METHODS OF USE

FILE REFERENCE: 4239-66903-02

CURRENT APPLICATION NUMBER: US/10/527,500

CURRENT FILING DATE: 2005-03-11

PRIOR APPLICATION NUMBER: PCT/US2003/029833

PRIOR FILING DATE: 2003-09-18

PRIOR FILING DATE: 2002-11-12

PRIOR FILING DATE: 2002-11-12

PRIOR FILING DATE: 2002-09-19

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patent in version 3.2

SEQ ID NO 7

TYPE: PRT

ORGANISM: Phlebotomus ariasi

US-10-527-500-7

Query Match 11.0%; Score 240.5; DB 9; Length 393;

Best Local Similarity 24.2%; Pred. No. 1.3e-12;

Matches 97; Conservative 59; Mismatches 167; Indels 77; Gaps 16;

Qy 39 EYDYKNNVPSDIDQWHDKIFVTMLRYNGVPSL--NVISKVGGDGGPILQP----- 87

Db 24 EYAKNITPEGIDQASYN-----ENSIPTAFVHDALSKKIIIAIPRLYPOVPTLTLQ 77

Qy 88 ----YEDWS--FAYDDCSGIIVASAKLAIDKCDRLWLDGLV-----NNTQPMCSKLL 136

Db 78 DTTKHPERSPLEKPEFGSKLTSVQPMLEDCRRUWIDVGQVEYKGEQYKPKNPAIL 137

Qy 137 TFDLTSQL--LKQVEIPHVDVAVNATTKGRLSSLAQSLDNTNMTWYIADKGBGL 194

Db 138 AYDLTKDNPYEDIRYELPINIAGNIQFGGFTVDVTPNKEGC--GKTFIYITNFDNTL 194

Qy 195 IVYHNSDDSFHRLTNTFP--DYDPKFTKMTIDGESYTAQDGSGLM-----SPMTN-LYY 248

Db 195 IYVDQEKDSWKISHGSKPEHESNFH---NGAQYKYKAGIFGITLGDREDPEGRNPAY 251

Qy 249 SPVASTSLYYVNTQFRTSDYQNDI-----HYEGVQNLDTQSSAKVSKVSGVLPFG 301

Db 252 LGSSTKLFEVSEALKKKGAKFPVRLGDRGHTFAIALVYD-----PKTKVIFPA 303

Qy 302 LVGDSALGWCNEHRTLERHNRITVAQSDTLQMIASMKIEXAPHVIPFDYI---NREY 358

Db 304 ESDRSQISQWNTQKPLNHN-----TDVIYASSKF-----IFGTDIQIDSQ 346

Qy 359 ILVLSNMQMNVNDFDVFNFRIMANVNELLNTRCE 398

Db 347 LWFLNSGQPIDNLKLTFOKPHIRLARVDTKNSIRTRCE 386

RESULT 5

US-10-533-811-23

Sequence 23, Application US/10533811

Publication No. US20060051364A1

GENERAL INFORMATION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS

APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND

APPLICANT: HUMAN SERVICES

APPLICANT: Valenzuela, Jesus G.

APPLICANT: Ribeiro, Jose M.C.

APPLICANT: Barral, Aldina

APPLICANT: Netto, Manoel

APPLICANT: Brodskyn, Claudia

APPLICANT: Gomes, Regis

TITLE OF INVENTION: LU. LONGIPALPIS POLYPEPTIDES AND METHODS OF USE

FILE REFERENCE: 4239-67028-08

CURRENT APPLICATION NUMBER: US/10/533,811

CURRENT FILING DATE: 2005-04-29

PRIOR APPLICATION NUMBER: US 60/422,303

PRIOR FILING DATE: 2002-10-29

PRIOR APPLICATION NUMBER: PCT/US2003/034453

PRIOR FILING DATE: 2003-10-29

NUMBER OF SEQ ID NOS: 73

SOFTWARE: Patent in version 3.3

SEQ ID NO 23

LENGTH: 412

TYPE: PRT

ORGANISM: Lutzomyia longipalpis

US-10-533-811-23

Query Match 11.0%; Score 240.5; DB 9; Length 412;

Best Local Similarity 24.7%; Pred. No. 1.4e-12;

Matches 103; Conservative 69; Mismatches 170; Indels 75; Gaps 19;

Qy 33 DAILSGEYDYKNYPSD-IDQWHDKIFVTMLRYN-GVPSLNVISKVGGDGGPILQYP 89

Db 33 DGLTDDYNNPKFNPTGLAVDPEGYRLFIAPRRKPKVPYTVAEALNMVMPGFP-VERAP 91

Qy 90 DWSPAKYDDCSG-----IVSASKLAIDKCDRLWLDGLVNNT-----QPMCSKLLTF 138

Db 92 --SEKPKFKNGEGKDLVNVYQPVIDDCLRLWLDIGKVEYTGADADQYKPKGPTLIA 149

Qy 139 DLTTSQL--LKQVEIPHVDV-----AVNATTKGRLSSLAQSLDNTNMTWYI 186

Db 150 DLKXDHTEPHRPEIPDLYSSQVEFGGFAVDVVNTKG-----DC---TESPYL 196

Qy 187 ADEKGEGLIVYHNSDDSFHRLTNTFDYDPKFTKMTIDGESYTAQDGSGLMSPMTN 246

Db 197 TNFDKNSLIVYDEYTKKAWKFTDKTFEADKESTSYSGEOMKYKGLGFGALGD-RDEM 255

Qy 247 YVSPV-----ASTSLYYVNTQFRTSDYQON-DIHYEGVQNLDTQSSAKVSKVSGVLP 300

Db 256 GHRPACYTAGSTKYVSVNTKELTENGOLNPLH--GDRCKYTDALAYDPEHKVLYF 313

Qy 301 GLVDSALGWCNEHRTLERHNRITVAOS-----DETQMIASMKIEXAPHVIPFDYI 354

Db 314 AESDSRQVSCWNVNMLKPDNTDVFSSARFTFGTDILVDSKGLMWINANGHPVDEQ-- 371

Qy 355 NREYILVLSNMQMNVNDFDVFNFRIMANVNELLNTRCENPDNDRTPFKISI 411

Db 372 -----EKIWKH-----RFVNRKIRIMKVTERVFKYSRC-NP-NYKPKKELEV 412

RESULT 6

US-10-527-500-49

Sequence 49, Application US/10527500

Publication No. US20060004186A1

GENERAL INFORMATION:

```
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; APPLICANT: Kamhawi, Shaden
; APPLICANT: Belkaid, Yasmine
; APPLICANT: Fischner, Laurent Bernard
; APPLICANT: Audonnet, Jean-Cristophe
; APPLICANT: Milward, Francis William
; TITLE OF INVENTION: P. ARIASI POLYPEPTIDES AND P. PERNICIOSUS POLYPEPTIDES AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 4239-66903-02
; CURRENT APPLICATION NUMBER: US/10/527,500
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: PCT/US2003/029833
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US 60/425,852
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/412,327
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Phlebotomus perniciosus
US-10-527-500-49

Query Match          9.8%; Score 214; DB 9; Length 393;
Best Local Similarity 23.3%; Pred. No. 2.4e-10;
Matches 97; Conservative 60; Mismatches 151; Indels 108; Gaps 19;

Qy 39 EYDKNNYPSDIDQWHDKIFVTMLRYNGV-PSSLNV-----ISKVGDGGPLL 85
Db 24 EYAWKN-----ISYEGVDPALFNIDNIITPGFVHDAINKKIFIAVPRR 66
Qy 86 QP-----YPDWS--FAKYDDCSGIVSASKLAIDKCDRLWLVDGLVN----- 125
Db 67 SPQIPFTLTDLTTKHPERSPLSKFPGSKDLINVYQPVIDECHRLWIADVGRVYKGD 126
Qy 126 NTQPMCSKLLTFLDTSQL--LKQVEIPHDVAVNATTKGRSLSSLAQSLDCNTN---- 179
Db 127 QKYPNQNAVLIAYDLTKENYPEIHRYPEIPSKIAGSNTIPFG---GFAVDV---TNPKEG 179
Qy 180 -SDTMVVIADKGBGLVYHNSDDSFHRLTSNTF--DYDPKFTQWTTIDGSSYTAQDGISG 236
Db 180 CGKTFVITPFDNTLIVYDQEKDQSWKISHGSKPEHD---STLSHDGQYKYRVGLFG 236
Qy 237 MAL---SPMTNN-LYYSFVASTSLYYVNTF-----QRTSDYQQNDIHYEGVQNILDT 285
Db 237 ITLGDRLPEGNRPAYIAGSSTKLFEISTKILKEGAKFDPVNLGNRGPHTEAVALVYD- 295
Qy 286 QSSAKVSKGVLFFGLVGSALCGWNEHRTLEHNRITRTVAQSDETLQMIASMKIEXAP 345
Db 296 -----PKTKVIFFAESDSRQVSCWNTQKPLNHN-----TDVIFASAKF----- 334
Qy 346 HVPIFDRIYI---NREYILVLSNKKQKMWVNDNFDDVNERIMANVNELINTRCE 398
Db 335 ---IYGSISVDSSESLQWFLSTGTHPPINLKLTFDKPHIRLMRVDTAKAIRTRCE 387

RESULT 7
US-10-533-811-63
; Sequence 63, Application US/10533811
; Publication No. US20060051364A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Ribeiro, Jose M.C.
; APPLICANT: Barrai, Aldina

; APPLICANT: Netto, Manoel
; APPLICANT: Brodskyn, Claudia
; APPLICANT: Gomes, Regis
; TITLE OF INVENTION: LU. LONGIPALPIS POLYPEPTIDES AND METHODS OF USE
; FILE REFERENCE: 4239-67028-08
; CURRENT APPLICATION NUMBER: US/10/533,811
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/422,303
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/US2003/034453
; PRIOR FILING DATE: 2003-10-29
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Latzomyia longipalpis
US-10-533-811-63

Query Match          8.4%; Score 184; DB 9; Length 399;
Best Local Similarity 22.6%; Pred. No. 8.5e-08;
Matches 97; Conservative 61; Mismatches 168; Indels 104; Gaps 20;

Qy 16 HEWKFFDYDFGSDERRQDAILSGEYDYKNYPSDI--DQWHDKIFVTMLR-YNGVPSLN 72
Db 24 YKWKQLLY-----NNVTPGSYNPDNMI STAFAYDAEGEKLFLAVPRKLPVRYPTLA 74
Qy 73 VISKK-----VGDGGLLQPPYDWSFAKYDDCSGIVSASKLAIDKCDRLWLVDGLVN-- 125
Db 75 EVDTONSLGVKGKHSPLLN-----KFSGHKTGKELTSIYQPVIDDCRRLWVVDIGSVEYR 129
Qy 126 ----NTQPMCSKLLTFLDTSQLLKQVRIPHDV-----AVNATTGK 163
Db 130 SRGAKDYPSHRPAIVAYD-----LKQPNVPEVRYVFPTRLVEKPTYFGGFAVDVANPK 183
Qy 164 GRUSSLAOSLDCNTNSDTWVIADKGLVIV--HNSDDSFHRLTSNTFDYDPKTKMT 222
Db 184 G-----DC---SETFVITNFGALFIYDHKKQDSWN-VTHPTFKAB-RPTKFD 238
Qy 223 IDGESYTAQDGISGMAL-----SPMTNNLYSPVASTSLYYVNTFQRTSDYQQNDIHYEG 278
Db 229 YGKEYEYFAGIFGIIIGDRDSEGNRPAYLAGSAIKVSVNTKELKQGGKLN-ELLG 287
Qy 279 VQNILDTQSSAKVSKGVLFFGLVGSALCGWNEHRTLEHNRITRTVAQSDETLQMIASG 338
Db 288 NRKYNDAIALAYDPKTKVIFFAEANTKQVSCWN-----TQKMPLRM 329
Qy 339 KIKEAXPHVPIFDRIYI-----NREYILVLSNKKQKMWVND--FNFDVNERIMN-ANV 388
Db 330 KNTDV---VYTSRFRVFGTDISVDSKGLWFMWSNGPPIRKSEKFKYDFRYRLMRIMDT 386
Qy 389 NELILNTRCE 398
Db 387 QEAIAGTACD 396
```


APPLICANT: DANIELS, JUSTIN
APPLICANT: GOEBEL, WERNER
APPLICANT: KREFT, JURGEN
APPLICANT: KUHN, MICHAEL
APPLICANT: NG, EVA
APPLICANT: VAZQUEZ-BOLAND, ANTONIO
APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
APPLICANT: GARRIDO-GARCIA, PATRICIA
APPLICANT: TIERREZ-MARTINEZ, ALBERTO
APPLICANT: AMEND, ALEXANDRA
APPLICANT: CHAKRABORTY, TRINAD
APPLICANT: DOMANN, EUGEN
APPLICANT: HAIN, THORSTEN
APPLICANT: BERCHE, PATRICK
APPLICANT: CHARBIT, ALAIN
APPLICANT: DURANT, LIONEL
APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
APPLICANT: BAQUERO, FERNANDO
APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
APPLICANT: GOMEZ-LOPEZ, NURIA
APPLICANT: MADUENIO, ENCARN
APPLICANT: PABLOS, BETRIZ DE
APPLICANT: WEHLAND, JURGEN
APPLICANT: KARST, UWE
APPLICANT: ENTIAN, KARL-DIETER
APPLICANT: HAUF, JORG
APPLICANT: ROSE, MATTHIAS
APPLICANT: VOSS, HAMUT
TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
FILE REFERENCE: 05394.0018-02
CURRENT APPLICATION NUMBER: US/11/045.004
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: 10/637,657
PRIOR FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: 10/257,023
PRIOR FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: PCT/FR01/01118
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: FR 00/04,629
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 2854
SOFTWARE: PatentIn version 3.3
SEQ ID NO 34
LENGTH: 1530
TYPE: PRT
ORGANISM: Listeria monocytogenes
US-11-045-004-34

Query Match 5.2%; Score 113.5; DB 11; Length 1530;
Best Local Similarity 20.8%; Pred. No. 0.55;
Matches 106; Conservative 79; Mismatches 182; Indels 143; Gaps 32;

Qy 3 LRGSLSKSLPLHEW-KFFDYDFGSDRRQDAI-----LSGEYDYKNN----- 45
Db 522 LNGDS-----SWEKGFQINFRDITGQHVITYKTVQNPSTHTSGDNEYTNATIKT 572

Qy 46 ---YPSDID-QWHDKIFVTMLRYNGVSPSSLVNISKVGGGLLPQPPDWSFAKYDDCSG 101
Db 573 DTAERASDSTKWIDKVIDADGYKNG-----VFNYKTGE-----IEWKL1-FNDSSK 617

Qy 102 IVSASKLAID---KCDRLWVLDGLVNTQPMCSPL-----LTFDLT-----TSOL 145
Db 618 LI--SKPTIEDSLNSGQTFIQDSBIHKIDLSATPQVGEIAPPENYDVTFTKNGNEQM 675

Qy 146 LKQVEIP--HDVAVNATT-----GKRLSSLAVALQDNCNTNSDTWVY 185
Db 676 LITFKKLIHPVEVYTKPGVITKPLYNKAVISDGEVLADYEAVIDDNANK-----Y 731

Qy 186 I---ADEKGEGL--IVVHNSDDSFHRLTSNTFDYDPKFTKMTIDGES---YTAQGISG- 236
Db 732 VNKSGEQVDNIDWEIYANQSGS---TVSNATVDTLTGQKLDTSIKVYKSQTSVTGK 788

Qy 237 -----MALSPMTNNLYSPVASTSLYYVNTPEQTSYQQNDIHYE-GVQNILDQSSA 289

Db 789 MLOESNMPISGCEYDLKTGVDESNLEVPQV-KFRNEINQSYVIKYQTAITLTSDETETA 847
Qy 290 KVVSKSVGLFFGLVGDSALGCWNEHRTLERHNIRT-VAQSD-----ETLQMIASMKIKEA 343
Db 848 QI--GNSVTF-----TGUNI-----TKGETEKTKIEVKIITGDTGTGCTGKIILN-KVDKA 897
Qy 344 XPHVPI-----FDRYINREYILVLSNKKMQQVNV-NDFNPDVNVFRINMANVNNELILNTRCE 398
Db 898 DESIPLEGATFDLYANDEKVDVDTQTDKNGVIEFDLIVGDDYTLKVSAPGCVTLPTASTE 957
Qy 399 NPD-----NDRTPFKIS--IHL 413
Db 958 NIQVKLEQDEKVVQVNMKEKPIKETGEVHL 987

RESULT 9
US-10-909-769-26
; Sequence 26, Application US/10909769
; Publication No. US20060024331A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Lin, Wei-Jen
; APPLICANT: Aoki, Kei Roger
; APPLICANT: Sachs, George
; TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteristics
; FILE REFERENCE: ALL80010-100 (ROI2003-146)
; CURRENT APPLICATION NUMBER: US/10/909,769
; CURRENT FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 829
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of HC
US-10-909-769-26

Query Match 5.0%; Score 108.5; DB 9; Length 829;
Best Local Similarity 20.2%; Pred. No. 0.62;
Matches 91; Conservative 80; Mismatches 168; Indels 111; Gaps 25;

Qy 14 ILHEMKFFDYDFGSDRRQDAIILSGEYDYKYNPSDIDQWHDKIFVTMLRYNGVSPSSLVN 73
Db 14 VASENSYNDNINTPKEIDDTVIS-----NNVENDLDQ-----VILNFNS-ESAPGL 60

Qy 74 ISKKVGDGGLLPQPPDWSFAKYDDCSGIYSASKLAIDKCDRLWVLDGLV-----NN--- 126
Db 61 SDEKLN-----LITQNDAYIPKYDS-NGTSDIEQHDVNLNVPFYLDQAKVPEGENNVNL 114

Qy 127 -----TQPMCSPLKLLTFDLTTSOLLKQVEIP-----HDVAVNATTCKGRLS----- 167
Db 115 TSSIDTALLEQPKIYTF--FSSEFINNVNPKVQAAFLVSWIQVLYVDFTFTEANQKSTVDK 172

Qy 168 ----SLAVQSLDCNTNSDTWVYIADEKGEGLIVHNSDDSFHRLTSN-TFYDYPKF---T 219
Db 173 IADISIVVPIGIALN-----IGNEAQKG-----NFKDALELLGAILLEFEPELLIPT 221

Qy 220 KMTIDGESYTAQDGISGMALSPMTNNL-----YSPVASTSLYYVNTPEQTSYQ 270
Db 222 ILVFTIKSFGLSSDNKNKVIKAINNALKERDEKWKVEYVFVSNWMTKINT-QFNKKEQ 280

Qy 271 QNDIHYEGVQNILDQSSAKVSKVGLFFGLVGDSALGCWNEHRTLERHNIRTVAQSD 330
Db 281 M----YQALQNV---NAIKTIIESK-----YNSY-TLEEKNELNKKYDIK 318

Qy 331 TLQMIASMKIKEAPHPVPIFDRIYNR---EYILVLSN--KMQKMNNDNFDD--VNFRI 383
Db 319 QIENELNKKVSIAMNNI---DRFLTSSISYLMKLINEVKINKUREYDENVKTYLLNVI 375

Qy 384 MNANV---NELILNTRCENPDNDRTPFKIS 410


```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-051-4

Query Match      4.6%; Score 99.5; DB 11; Length 2376;
Best Local Similarity 18.8%; Pred. No. 16;
Matches 78; Conservative 63; Mismatches 119; Indels 155; Gaps 18;

Qy 3 LRGSLSKSLPILHEWKFDD-----YDFGSDERRDQAILSGEYDYKNYPSPDID 51
Db 1170 IIRAVSKNKLNSMNFYEASPTDQELYIFDINGTHQYTVSLVTGDLNFSYND-- 1227
Qy 52 QWHDKIFVTMLRYNGVPSSLNVISKKVGDGGLLPQYPDMWSFAKYDDCSGIVSASKLAID 111
Db 1228 -----NDITAVTDSNGNTLRIRD----- 1246
Qy 112 KCDRLWLVDGLVNNTQPMCSKLLTFLDTSQLLKQVEIPHVDVAVNATTG-KGRLLSLSLA 170
Db 1247 -----PNRMPV-----RVVSPDNQVIMLTIGTNGCLKSMT 1276
Qy 171 VQSILDC-----NTNSDTMVIYADEKGBGLIVYHNSDDSFHRLTSTNPF-----DYD 215
Db 1277 AQGLELVFTYHGNSGLLATKSDGTGTTTFDYDSEG---RLTNVTFTPTGVVTVNLHGDM 1333
Qy 216 PKFTKMTIDGESYTAQDGSIGSMALSPMTNNLYSPVASTSLYYNTQFRTSDYQNDIH 275
Db 1334 ---KAITVDIESSREEDVS-----ITSNL-----SSIDSFTYVWQDLRNS-YQ---IG 1376
Qy 276 YEGVQNILDTSQSAKVSKSVGLVFFGLVGSALGCWNEHRTLERHNIR-----TVAQSDE 330
Db 1377 YDG-----SLRIIVASGL-----DSHYQTEPHVLGANTANPTVAKRNM 1413
Qy 331 TL-----QMIASMKIK--EAXPHVPIFDRIYINREVILVLSNMQKQVNNDFNFD 378
Db 1414 TLPGENQNLVEWFRKQEQAGKQVNVFGRKLRVNGRNLSSVDFDRTTKTEKIYDD 1468

RESULT 13
US-11-096-051-2
; Sequence 2, Application US/11096051
; Publication No. US20050244868A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacLachlan, Timothy K
; APPLICANT: Rastelli, Luca
; APPLICANT: Vernet, Corine
; APPLICANT: Ettenberg, Seth
; TITLE OF INVENTION: Ten-M3 Polypeptides and Polynucleotides and their Methods of Use
; FILE REFERENCE: Attorney Docket No. Cura 967
; CURRENT APPLICATION NUMBER: US/11/096,051
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: 10/038,854
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 10/455,772
; PRIOR FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: 60/557,978
; PRIOR FILING DATE: 2004-03-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 2715
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-096-051-2

Query Match      4.6%; Score 99.5; DB 11; Length 2715;
Best Local Similarity 18.8%; Pred. No. 19;
Matches 78; Conservative 63; Mismatches 119; Indels 155; Gaps 18;

Qy 3 LRGSLSKSLPILHEWKFDD-----YDFGSDERRDQAILSGEYDYKNYPSPDID 51
Db 1509 IIRAVSKNKLNSMNFYEASPTDQELYIFDINGTHQYTVSLVTGDLNFSYND-- 1566

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-525-567-4

Query Match      4.6%; Score 99.5; DB 11; Length 2376;
Best Local Similarity 18.8%; Pred. No. 16;
Matches 78; Conservative 63; Mismatches 119; Indels 155; Gaps 18;

Qy 3 LRGSLSKSLPILHEWKFDD-----YDFGSDERRDQAILSGEYDYKNYPSPDID 51
Db 1170 IIRAVSKNKLNSMNFYEASPTDQELYIFDINGTHQYTVSLVTGDLNFSYND-- 1227
Qy 52 QWHDKIFVTMLRYNGVPSSLNVISKKVGDGGLLPQYPDMWSFAKYDDCSGIVSASKLAID 111
Db 1228 -----NDITAVTDSNGNTLRIRD----- 1246
Qy 112 KCDRLWLVDGLVNNTQPMCSKLLTFLDTSQLLKQVEIPHVDVAVNATTG-KGRLLSLSLA 170
Db 1247 -----PNRMPV-----RVVSPDNQVIMLTIGTNGCLKSMT 1276
Qy 171 VQSILDC-----NTNSDTMVIYADEKGBGLIVYHNSDDSFHRLTSTNPF-----DYD 215
Db 1277 AQGLELVFTYHGNSGLLATKSDGTGTTTFDYDSEG---RLTNVTFTPTGVVTVNLHGDM 1333
Qy 216 PKFTKMTIDGESYTAQDGSIGSMALSPMTNNLYSPVASTSLYYNTQFRTSDYQNDIH 275
Db 1334 ---KAITVDIESSREEDVS-----ITSNL-----SSIDSFTYVWQDLRNS-YQ---IG 1376
Qy 276 YEGVQNILDTSQSAKVSKSVGLVFFGLVGSALGCWNEHRTLERHNIR-----TVAQSDE 330
Db 1377 YDG-----SLRIIVASGL-----DSHYQTEPHVLGANTANPTVAKRNM 1413
Qy 331 TL-----QMIASMKIK--EAXPHVPIFDRIYINREVILVLSNMQKQVNNDFNFD 378
Db 1414 TLPGENQNLVEWFRKQEQAGKQVNVFGRKLRVNGRNLSSVDFDRTTKTEKIYDD 1468

RESULT 14
US-10-525-567-4
; Sequence 146, Application US/10194487
; Publication No. US20060074226A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deanovers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colleen K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C312
; CURRENT APPLICATION NUMBER: US/10/194,487
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 146
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-487-146
```

